

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 31, 2003, 13:38:07 ; Search time 3280 Seconds
(without alignments)
3362.794 Million cell updates/sec

Title: US-09-944-884-2

Perfect score: 1992

Sequence: 1 MKEYVLLIFLALCSAKPFPS.....PATFRCVLSRMSVQLNGFM 379

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

`abase :

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16: em.fun.*
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41: em.htgo_other.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	1992	100.0	1184	9	AF316824	Homo sapi	AF316824 Homo sapi
2	1992	100.0	2454	6	AX400320	Sequence	AX400320 Sequence
3	1992	100.0	2454	6	AX454444	Sequence	AX454444 Sequence
4	1992	100.0	2454	6	AX464194	Sequence	AX464194 Sequence
5	1992	100.0	2454	6	AX490922	Sequence	AX490922 Sequence
6	1981	99.4	2466	9	AY029191	Homo sapi	AY029191 Homo sapi
7	1799	90.3	1165	10	AF316825	Mus muscu	AF316825 Mus muscu
8	1799	90.3	2325	10	BC034888	Mus muscu	BC034888 Mus muscu
9	1517	76.2	2089	9	AK027359	Homo sapi	AK027359 Homo sapi
10	1385	69.1	1903	9	AK000136	Homo sapi	AK000136 Homo sapi
11	1118	55.1	1634	5	AF247821	Oreochrom	AF247821 Oreochrom
12	1045	52.5	2960	5	AB037269	Xenopus l	AB037269 Xenopus l
13	1040	52.2	1107	6	A77048	Sequence	A77048 Sequence
14	1040	52.2	2446	10	RN017834	Rattus norv	UI7834 Rattus norv
15	1037	52.1	1964	10	MMFGI	M.musculus	X53928 M.musculus
16	1037	52.1	2383	10	BC005452	Mus muscu	BC005452 Mus muscu
17	1037	52.1	2390	10	BC019502	Mus muscu	BC019502 Mus muscu
18	1034	51.9	1104	6	AX148654	Sequence	AX148654 Sequence
19	1034	51.9	1685	6	AX146889	Sequence	AX146889 Sequence
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27	1034	51.9	2367	6	AX011750	Sequence	AX011750 Sequence
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29	1034	51.9	2422	9	BC004244	Homo sapi	BC004244 Homo sapi
30	1034	51.9	6321	6	AX281606	Sequence	AX281606 Sequence
31	1028	51.6	2294	4	AF035934	Equus cab	AF035934 Equus cab
32	1027	51.6	1110	4	AF034842	Ovis arle	AF034842 Ovis arle
33	1026	51.5	2372	10	MUSBIGLY	Mouse bigly	L20276 Mouse bigly
34	1024	51.4	2043	4	BOVBIGLY	Cow biglyca	L07953 Cow biglyca
35	1024	51.4	2249	9	AK094059	Homo sapi	AK094059 Homo sapi
36	1021	51.3	1474	4	CF083140	Canis fami	U83140 Canis fami
37	1019	51.2	2043	4	S82652	Bos taurus	S82652 Bos taurus
38	974	48.9	1837	5	AF125250	Coturnix	AF125250 Coturnix
39	969	48.6	1618	5	GDDECORIN	G. domestic	X63797 G. domestic
40	967	48.5	1492	4	AF125537	Sus scrof	AF125537 Sus scrof
41	963	48.4	1080	9	AF138300	Homo sapi	AF138300 Homo sapi
42	963	48.4	1771	9	BC005322	Homo sapi	BC005322 Homo sapi
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ALIGNMENTS

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AF316824	1184 bp	linear	PRI 20-APR-2000
LOCUS	1184 bp	mrna	
DEFINITION	Homo sapiens asporin precursor (ASP) mRNA, complete cds.		
ACCESSION	AF316824		
VERSION	AF316824.1		
KEYWORDS	GI:13625796		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Lorenzo P., Aspegren, A., Onnerfjord, P., Bayliss, M.T., Neame, P.J. and Heinigard, D.		
TITLE	Identification and characterization of asporin, a novel member of the leucine-rich repeat protein family closely related to decorin and biglycan		
JOURNAL	J. Biol. Chem. 276 (15), 12201-12211 (2001)		
MEDLINE	21192276		
PUBMED	11152692		
REFERENCE	2 (bases 1 to 1184)		
AUTHORS	Direct Submission		
TITLE	Submitted (26-OCT-2000) Cell and Molecular Biology, Lund University, BMC plan C12, Lund SE-221 84, Sweden		
JOURNAL	Location/Qualifiers		
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CDS	19. .1158		
	/gene="ASP"		
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	/product="asporin precursor"		
	/protein_id="AAK35161.1"		
	/db_xref="GI:13625797"		
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misc_feature	/note="by similarity; disulfide bond"		
	859. .861		
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BASE COUNT	412 a	225 c	220 g 327 t
ORIGIN			
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Pred. No.:	1.27e-166	Lengths:	1184
Score:	1992.00	Matches:	379

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Db      979  AATTCAATTCGAAGAGTGGAGTAATGACTTCTGTCCCAACAGTGCACCAAGATGAAGAA 1038
Qy      341  SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnPro 360
Db      1039 TCTTTATACAGTCAATAGTTATTATCAACACCCCGTGAATACCTGGGAATGCAACCT 1098
Qy      361  AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet 379
Db      1099 GCACACATTCGTGTGTTTGGACCAATGAGTGTTCAGCTTGGGAACCTTGGAAAG 1155

RESULT 2
AX400320 2454 bp DNA linear PAT 06-JUN-2002
LOCUS
DEFINITION Sequence 1 from Patent EP1191101.
ACCESSION AX400320
VERSION AX400320.1 GI:21336501
FEATURES
    source human.
    CE Homo sapiens
    ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1 Baker, K.P., Chen, J., Goddard, A., Gurney, A.L., Wood, W.I. and Yuan, J.
      Polypeptides and nucleic acids encoding the same
      Patent: EP 1191101-A 1 27-MAR-2002;
      Genentech, Inc. (US)
    Location/Qualifiers
        1..2454
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
BASE COUNT 835 a 432 c 417 g 770 t
ORIGIN

Alignment Scores:
Pred. No.: 3,1e-166 Length: 2454
Score: 1992.00 Matches: 379
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-944-884-2 (1-379) x AX400320 (1-2454)

Qy      1  MetLysGlnTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPhePheSer 20
Db      234  ATGAAGAGATGTGCTCTCTATTATTCCTGGCTTTGTGCTCTGCCAAACCTCTCTTTAGC 293
Qy      21  ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40
Db      294  CCTTCACATCGCACTGAAGATATGATGCTGAAGGATATGGAAGACACAGATGATGAT 353
Qy      41  AspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60
Db      354  GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413
Qy      61  ProArgSerHisPhePheProPheAspLeuPheProMetCysProPheGlyCysGlnCys 80
Db      414  CCAAGAGCCATTTTTCCTATGATCTCTTTCCATGATGCTCCATTTGGATGATGATGAT 473
Qy      81  TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100
Db      474  TATTCAGAGCTTGATACCTCTCAGATTTAGTTGACCTCAGTCCCAACCAACATTCCTCA 533
Qy      101  PheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluIleLysGluAsnAsp 120
Db      534  TTTGATACCTGAATGCTGTGATCTTCAAAACAATAAATAAGGAAATCAAGAAATGAT 593
Qy      121  PheLysGlyLeuThrSerLeuTyrGlyLeuIleLeuAsnAsnLysLeuThrLysIle 140
Db      594  TTTAAAGGACTCACTTCTCATTATGTTGCTGATCTGATCAACCAACCAAGCTTAACGAAT 653
Qy      141  HisProLysAlaPheLeuThrThrLysLysLeuArgArgLeuTyrLeuSerHisAsnGln 160

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Db      654  CACCCAAAAGCCCTTTCTAACCCAAAGAAAGTGTGCGAAGGCTGTATCTGTCCCAACATCAA 713
Qy      161  LeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180
Db      714  CTAAGTGAATACCACTTATCTTCCCAATCATTAGCAGACTCAGAAATCATGAAAT 773
Qy      181  LysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGlu 200
Db      774  AAAGTTAAGAAAATACAAAAGGACACATTCAAGAGGAATGAATGCTTTACACGTTTGGAA 833
Qy      201  MetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThr 220
Db      834  ATGAGTGCACACCTCTTGATAATATGGATAGAGCCAGGGGCATTTGAAGGGTGACG 893
Qy      221  ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProPro 240
Db      894  GTGTTCCATATCAGAAATTCAGAGAAGCAAACTGACCTCAGTCTCTAAAGGCTTTACCA 953
Qy      241  ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe 260
Db      954  ACTTTATTGGAGCTTCACTTAGATTATAATAAATTTCAACAGTGAACCTTGAGGATTT 1013
Qy      261  LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280
Db      1014  AAACGATACAAAGAACTACAAAGCTGGGCTAGGAACCAACAAATCAGAGATATCGAA 1073
Qy      281  AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnAsnLysLeu 300
Db      1074  AATGGGAGTCTTCTCAACATACCACTGTCGAGAGAAATACATTTGGAAAACAATAACTA 1133
Qy      301  LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleLeuPheLeuHisSer 320
Db      1134  AAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATAATCTTCTCTCATCT 1193
Qy      321  AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys 340
Db      1194  AATTCATTCGAAGTGGGAGTAAATGACTTCTGCCAAGTGCACCAAGATGAAGAA 1253
Qy      341  SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnPro 360
Db      1254  TCTTTATACAGTGCATTAAGTTATTCAACAACCCGCGTGAATACTGGGAAATGCAACCT 1313
Qy      361  AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet 379
Db      1314  GCAACATTCCTGTGTGTTTGGAGCAGAATGAGTGTTCAGCTTGGGAACTTTGGAATG 1370

RESULT 3
AX454444 2454 bp DNA linear PAT 06-JUL-2002
LOCUS
DEFINITION Sequence 29 from Patent WO0208284.
ACCESSION AX454444
VERSION AX454444.1 GI:21713846
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
      Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
      Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.N., Wood, W.I.
      and Ye, W.
      Compositions and methods for the diagnosis and treatment of
      disorders involving angiogenesis
      Patent: WO 0208284-A 29 31-JAN-2002;
      Genentech, Inc. (US) ; Baker, Kevin-P. (US) ; Ferrara, Napoleone
      (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
      Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
      Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
      ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
      Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
      I. (US)
      Location/Qualifiers
FEATURES

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Score: 1992.00 Matches: 379
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-944-884-2 (1-379) x AX454444 (1-2454)

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Qy 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAAspThrAspAsp 40
Db 294 CCTTCACATCGCACTGAAGAATATGATGCTGAGGATATGGAGACACAGATGATGAT 353

Qy 41 AspAspAspAspAspAspAspAspGluAAspAsnSerLeuPheProThrArgGlu 60
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Qy 61 ProArgSerHisPhePheProPheAspLeuPheProMetCysProPheGlyCysGlnCys 80
Db 414 CCAAGAGGCATTTTTTCCATTTGATCTGTTTCCAATGTGCTCATTTGGATGTCAGTGC 473

Qy 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100
Db 474 TATTCAGAGTGTACATGCTCAGATTAGTTGACTCAGTCCCACCAACATGCCA 533

Qy 101 PheAspThrArgMetLeuAspLeuGlnAsnLysLysLysGluIleLysGluAsnAsp 120
Db 534 TTGTATCTCGAATGCTTGTATCTTCAAACAATAAAAATTAAGGAATCAAGAAAAATGAT 593

Qy 121 PheLysGlyLeuThrSerLeuTyrGlyLeuLeuLeuAsnAsnLysLeuThrLysIle 140
Db 594 TTTAAAGGACTCACCTTATGCTGATGCTGCAACAACAACAGCTAACCAAGAT 653

Qy 141 HisProLysAlaPheLeuThrThrLysLysLeuArgLeuTyrLeuSerHisAsnGln 160
Db 654 CACCACAAAGCCTTCTACACCAAGAGTTCGAAGCTGTATCTGCCCAACATCAA 713

Qy 161 LeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180
Db 714 CTAAAGTGAATACCACTTAATCTCCCAATCATTTAGCAGAACTCAGAAATTCATGAAAT 773

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Db 774 AAGTTAAGAAATCAAAAGACACATTCAAAGGAATGAATGCTTTACACGTTTGGAA 833

Qy 201 MetSerAlaAsnProLeuAspAsnGlnGlyProGlyAlaPheGluGlyValThr 220
Db 834 ATGAGTGCAAAACCTTCTGATTAATGGGATAGACCCAGGGGATTTGAAGGGGTGACG 893

Qy 221 ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProPro 240
Db 894 GTGTTCCATATCAGAAATTCGAGAACAAACAGTACCTCAGTTCTTAAAGGCTTACCACCA 953

Qy 241 ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe 260
Db 954 ACTTTATTTGGAGCTTCACTTAGATTATATAATAATTTCAACAGTGGAACTTTGAGGATTTT 1013

Qy 261 LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280
Db 1014 AAACGATCAAGAACTACAAGGCTGGGCTAGCAACAACAATAATACACAGATATATCGAA 1073

Qy 281 AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnAsnLysLeu 300

Db 1074 AATGGAGCTTTGCTAAACATACACGCTGTGAGAAATACATTTGGAAACAAATAAACA 1133

Qy 301 LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSer 320
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Qy 321 AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys 340
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RESULT 4
AX464194 2454 bp DNA linear PAT 16-JUL-2002
LOCUS AX464194
DEFINITION Sequence 327 from Patent WO0140466.
ACCESSION AX464194
VERSION AX464194.1 GI:21899113
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 Baker,K.P., Beresini,M., DeForge,L., Desnoyers,L., Filvaroff,E.,
Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Wood,W.L. and Zhang,Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
same
Patent: WO 0140466-A 327 07-JUN-2001;
Genentech Inc. (US)

FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 835 a 432 c 417 g 770 t
ORIGIN

Alignment Scores:
Pred. No.: 3.le-166 Length: 2454
Score: 1992.00 Matches: 379
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-944-884-2 (1-379) x AX464194 (1-2454)

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Qy 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAAspThrAspAsp 40
Db 294 CCTTCACATCGCACTGAAGAATATGATGCTGAGGATATGGAGACACAGATGATGAT 353

Qy 41 AspAspAspAspAspAspAspAspGluAAspAsnSerLeuPheProThrArgGlu 60
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ACCESSION AX490922
VERSION AX490922.1 GI:22323798
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SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,

Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 0200690-A 29 03-JAN-2002;
Genentech, Inc. (US)
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 DEFINITION complete cds.
 ACCESSION BC034888
 VERSION BC034888.1 GI:22028224
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 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Strausberg, R.
 Direct Submission
 Submitted (29-JUL-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapsb-remail.nih.gov
 Tissue Procurement: Marcello Bento Soares, Ph.D.
 cDNA Library Preparation: Soares Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
 Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
 Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
 Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Stott,
 Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
 George Yang, Scott Zuyderduyn, Marco Marra.
 Clone distribution: MGC clone distribution information can be found
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 This clone was selected for full length sequencing because it
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VERSION AK000136.1 GI:7020026
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REFERENCE 1 (sites)
Kawabata,A., Hikiiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 1903)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Department of Virology; Shirokane-dai, 4-6-1,
Minato-ku, Tokyo 108-8639, Japan (E-mail:cdna@ims.u-tokyo.ac.jp,
Tel:81-3-5449-5286, Fax:81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry for Japan; cDNA full insert
sequencing; Research Association for Biotechnology; cDNA library
construction, 5'- 3'-end one pass sequencing; Department of
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University of Tokyo (partly supported by Science and Technology
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VERSION	AB037269.1	GI:6759314
KEYWORDS	biglycan.	
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ORGANISM	Xenopus laevis	
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AUTHORS	1 (bases 1 to 2960)	
TITLE	Goto, T. and Kubota, H.Y.	
JOURNAL	CDNA of biglycan of Xenopus laevis	
REFERENCE	Published Only in DataBase (2000)	
AUTHORS	2 (bases 1 to 2960)	
TITLE	Goto, T. and Kubota, H.Y.	
JOURNAL	Direct Submission	
FEATURES	Submitted (20-JAN-2000) Toshiyasu Goto, Graduate School of Science, Kyoto University, Department of Zoology; Sakyo-Ku, Kyoto 606-8502, Japan (E-mail:goto@develop.zool.kyoto-u.ac.jp, tel: +81-75-753-4082, Fax: +81-75-753-4080)	
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BASE COUNT	859 a 667 c 652 g 782 t	
ORIGIN		
Alignment Scores:		
Pred. No.:	1,21e-82	Length: 2960
Score:	1045.50	Matches: 195
ent Similarity:	74.57%	Conservative: 63
Local Similarity:	56.36%	Mismatches: 69
Query Match:	52.48%	Indels: 19
DB:	5	Gaps: 2
US-09-944-884-2 (1-379) x AB037269 (1-2960)		
Qy	51 GluAspAsnSerLeuPhePro-----	-----ThrArgGluPro 61
	::: :: ::	
Db	330 GAGGATTCGGGATTTTTCATCGGACGATGGAATGGCTATGATCAAGATGAGGAGCGCT 389	
Qy	62 Arg-SerHisPhePhe-ProPheAspLeuPhePro-----	-----M 73
	:: ::	::
Db	390 CGGAGTAGGTCCTACCTACTGAGAGATTCAGAGATGTGGTTGCCACCTATGGATT 449	
Qy	73 etCysProPheGlyCysGlnCysTyrSerArgValValHisCysSerAspLeuGlyLeuT 93	
	:: :: ::	
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Qy	93 hrSerValProThrAsnIlePhePheAspThrArgMetLeuAspLeuGlnAsnLysI 113	
	:: :: ::	
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113	lelycsluilelysGluAsnAspPheLysGlyLeuThrSerLeuThrGlyLeuLeuA	133
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930	GCATCCCAAAAGTCTTCCAAGCACCCCTAATCAGCTTCACTTGACACACAAAGATCC	989
253	erThrValGluLeuGluAspPheLysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyA	273
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313	euGlnIlellePheLeuHisSerAsnSerIleAlaArgValGlyValAsnAspPheCysP	333
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ACCESSION	A77048	
VERSION	A77048.1	GI:6088837
KEYWORDS	unidentified.	
SOURCE	unidentified	
ORGANISM	unclassified.	
REFERENCE	1 (bases 1 to 1107)	
AUTHORS	Koops, A. and Hasenoeuhl, R. D.	
TITLE	USE OF CHONDROITIN SULPHATE, PROTEOGLYCANS FOR PROTECTION OF NEURONS	
JOURNAL	Patent: EP 0686397-A 1 13-DEC-1995;	
FEATURES	BOEHRINGER MANNHEIM GMBH (DE)	
	Location/Qualifiers	

[illegible]


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BASE COUNT 426 a 609 c 421 g 508 t
ORIGIN
Alignment Scores:
Pred. No.: 3,73e-82 Length: 1964
Score: 1037.50 Matches: 198
Percent Similarity: 70.37% Conservative: 68
Best Local Similarity: 52.38% Mismatches: 93
Gap Match: 19 Indels: 19
Gaps: 3
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US-09-944-884-2 (1-379) x MPMGI (1-1964)

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Qy 20 SerProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 39
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367 GACACCACCTTCAGGTGCCCGACCTGGAC-----TCTGTACACACCTACC-- 411
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862 AAGCTCAATTACCTGGCCATCTCAGAGGCCAGCTCACTGCGATCCCAAGATCTCCCT 921
Qy 240 ProThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuAsp 259
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922 GAGACCTGAACGAACCTTACCTGGACCACACAAATCCAGGCTATTGAGTTGGAGGAC 981
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Search completed: May 31, 2003, 16:40:04
Job time : 3293 secs

GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: May 31, 2003, 13:44:02 : Search time 1779 Seconds
(without alignments)
3450.303 Million cell updates/sec

Title: US-09-944-884-2
Perfect score: 1992
Sequence: 1 MREYVLLLELALCSAKPFSS.....PATRCVLSRMSVOLGNFGM 379

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO.spool/US09944884/runat_27052003_150250_7733/app_query.fasta_1.519
-DB=EST -QPM=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pcpt -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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Database : EST:
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14: gb_est5:*
15: em_estfun:*
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27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1790	89.9	2302	11	AK014504	AK014504 Mus muscu
2	1112	55.8	926	14	BQ960688	BQ960688 AGENCOURT
3	1035.5	52.0	695	10	AM608047	AM608047 RC3-LT002
4	978	49.1	533	9	AL598934	AL598934 DKEZ313F
5	922.5	46.3	1159	12	BF164270	BF164270 601773027
6	912	45.8	641	10	BE374603	BE374603 601225391
7	911	45.7	568	9	AI006670	AI006670 ue16b10.Y
8	893	44.8	936	14	BQ882271	BQ882271 AGENCOURT
9	845	42.4	592	9	AL600795	AL600795 DKEZP313E
10	822	41.3	839	14	BQ942694	BQ942694 AGENCOURT
11	818	41.1	865	9	AI789337	AI789337 uk53H09.Y
C 12	808.5	40.6	995	9	AL568847	AL568847 AL568847
C 13	804.5	40.4	879	9	AL571404	AL571404 AL571404
14	797	40.0	974	9	AL541759	AL541759 AL541759
15	777	39.0	955	14	BQ708510	BQ708510 AGENCOURT
C 16	760.5	38.2	824	9	AL571461	AL571461 AL571461
C 17	732.5	36.8	956	9	AL541055	AL541055 AL541055
18	727	36.5	996	12	BG111541	BG111541 602282864
19	720.5	36.2	771	9	AU118599	AU118599 AU118599
20	720	36.1	943	14	BQ900541	BQ900541 AGENCOURT
21	717.5	36.0	1078	14	BM807399	BM807399 AGENCOURT
22	712.5	35.8	883	13	BI827510	BI827510 603073959
C 23	712	35.7	923	14	BQ896057	BQ896057 AGENCOURT
24	707.5	35.5	827	13	BI182181	BI182181 UNL-P-FN-
25	705.5	35.4	897	12	BG674278	BG674278 602620247
26	698.5	35.1	943	14	BQ941521	BQ941521 AGENCOURT
27	694.5	34.9	850	13	BI455572	BI455572 603174818
28	692.5	34.8	1039	9	AL540886	AL540886 AL540886
29	690	34.6	663	9	AL047009	AL047009 DKEZP386M
30	686.5	34.5	957	9	AL540527	AL540527 AL540527
31	683.5	34.3	855	13	BI562281	BI562281 603255412
32	681.5	34.2	762	12	BG671736	BG671736 DRNBX807
33	681	34.2	821	12	BG678167	BG678167 602625946
34	678.5	34.1	879	14	BQ717417	BQ717417 AGENCOURT
35	678.5	34.1	897	9	AL543453	AL543453 AL543453
36	676	33.9	885	14	BQ668720	BQ668720 AGENCOURT
37	673.5	33.8	806	13	BI918450	BI918450 603176289
38	673	33.8	632	10	AW961537	AW961537 EST373609
39	666	33.4	864	14	BQ897542	BQ897542 AGENCOURT
40	662	33.2	865	14	BQ889362	BQ889362 AGENCOURT
41	661	33.2	850	14	BM720684	BM720684 UI-E-E00-
42	661	33.2	901	9	AL541040	AL541040 AL541040
43	659.5	33.1	947	9	AL541056	AL541056 AL541056
44	659.5	33.1	1060	9	AL524134	AL524134 AL524134
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ALIGNMENTS

RESULT 1
AK014504
LOCUS
DEFINITION AK014504 2302 bp mRNA linear HTC 19-JAN-2002
Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4631401G09:asporin, full insert sequence.

ACCESSION AK014504.1 GI:12852406
VERSION
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) 0 day neonate skin cDNA to mRNA, clone.lib:RIKEN full-length enriched mouse cDNA library
clone:4631401G09.

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Muridae; Sciurognathi; Muridae; Mus.

REFERENCE 1

AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS
---------	-------	---------	---------	--------	-----------	---------

Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

REFERENCE AUTHORS	TITLE	JOURNAL MEDLINE PUBMED	REFERENCE AUTHORS
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normalize and subtract of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159

REFERENCE
AUTHORS

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
Riken integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
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TITLE
JURNAL
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PUBMED
REFERENCE
AUTHORS

TITLE
JOURNAL
MEDLINE
PUBMED
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AUTHORS

5 (bases 1 to 2302)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, H., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sorabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toyota, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)


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Qy 156 LeuSerHisAsnGlnLeuSerGlu-IleProLeuAsn-LeuProLysSerLeuAlaGluL 175
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Qy 175 euArgIleHisGluAsnLysValLysLysIleGlnLysAspThrPheLysGlyMetAsnA 195
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Db 538 CTTTACATGCTCGGACACTGAGTGCAAACTCTTGAGCAACAAACAGATAGAACAG 597
Qy 214 lyAlaPhe-GluGlyValThrValPheHisIleArgIleAla-GluAlaLysLeuThr-S 233
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Qy 251 sileSerThrVal---GluLeuGluAspPheLysArgTyrLysGluLeu-GlnArgLeuG 270
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Qy 290 alArgGluIleHisLeuGluAsnAsnLysLeu-----300
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Db 918 -----TGCACAGACACAAACGACGCGCCACACGCGGCATCATCACTACGCGCG 966
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RESULT 6
BE374603
LOCUS 601225391F1 NCI_CGAP_Mam1 Mus musculus cdna linear EST 21-JUL-2000
DEFINITION mRNA sequence.
ACCESSION BE374603
VERSION BE374603.1 GI:9319966
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryote; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 641)
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
```

```
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLA8740 row: f column: 23
High quality sequence stop: 602.
Location/Qualifiers
1..641
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3583510"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 230 a 117 c 131 g 162 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 8,18e-99 Length: 641
Score: 912.00 Matches: 189
Percent Similarity: 94.37% Conservative: 12
Best Local Similarity: 88.73% Mismatches: 10
Query Match: 45.78% Indels: 5
Db: 1 Gaps: 1
US-09-944-884-2 (1-379) x BE374603 (1-641)
Qy 162 SerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisLysLeuLys 181
Db 2 AGTGAATTCCTCACTTAACTCTCCCAAACTATTAGCAAGACTCAGAAATTCATGATATAA 61
Qy 182 ValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGluMet 201
Db 62 GTTAAGAAGATACAAAAGGACACAGCTTCAAGGGAATGAATGCTTTACATGTTTGAATG 121
Qy 202 SerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThrVal 221
Db 122 AGTCAAAACCTCTTGAGAACACAGCGGATAGAACAGGGGCATTTGAAGGGGTGACAGTA 181
Qy 222 PheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProProThr 241
Db 182 TTCCATATCAGATCGCTGAAGCAAACTAACCCTCAATTCCAAAGGCTTACCACCAACT 241
Qy 242 LeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPheLys 261
Db 242 TTGCTGGAGCTTCATTTAGATTTTAAATAAATTTCAACGGTGAAGATCTTAA 301
Qy 262 ArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGluAsn 281
Db 302 CGGTACAGGGAACCTCAAAAGCTGGTCTTGAACAAACAGAAATCACAGATATTGAAAT 361
Qy 282 GlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnAsnLysLeuLys 301
Db 362 GGAACCTT-GCTAATATATACACGCTGTGAGAGAGATACACTTGGGAACAAATAAATA 420
Qy 302 LysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSerAsn 321
Db 421 AAATCCCTTCAGGATTCACAGAGTGTGAATACCTCCAGATAATCTCTTCATTATAAT 480
Qy 322 SerIleAlaArgValGlyValAsnAspPheCysProThr-ValProLysMetLysLysSe 341
Db 481 TCAATGTCAAAGTGGGAGTGAATGACTTCTGTCCAACAGNTGCCAAAGATGAAGAAATC 540
Qy 341 rLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnProAl 361
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLA8740 row: f column: 23
High quality sequence stop: 602.

FEATURES

source
1..641

/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3583510"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

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Db      541 TTTATACGTGCAATAGTTTATTCACAAACCAATGAAGTACTGGGAATACA-CCTGC 599
QY      361 aThrPheArgCysValLeuSerArgMetSerValGln 373
Db      600 A---CATTCGTGTGTTCTGTG---CGAATGAGTGTCAG 631

RESULT 7
AI006670
LOCUS   568 bp mRNA linear EST 12-JUN-1998
DEFINITION
ue16b10.y1 Sugano mouse embryo mewa Mus musculus cDNA clone
IMAGE:1480507 5' similar to SW:PGSI_HUMAN P21810 BONE/CARTILAGE
PROTEOLYCAN I PRECURSOR ;, mRNA sequence.
ACCESSION
AI006670
VERSION 1 GI:3216279
KEYWORDS
SOURCE house mouse:
ORGANISM Mus musculus
REFERENCE
1 (bases 1 to 568)
AUTHORS
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Willson,R. and
Waterston,R.
TITLE The WashU-HMML-Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Maria M/Mouse EST Project
WashU-HMML Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:928863
Possible reversed clone: similarity on wrong strand
Seq primer: primer name ambiguous
High quality sequence stop: 371.
FEATURES
source
1. 568
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1480507"
/dev_stage="embryo, 14 dpc"
/lab_host="DH10B"
/notes="Vector: pME18S-FL3; Site 1: DraIII (CACTGTGTG);
Site 2: DraIII (CACCATCTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGCCCTTTTCTTTTCTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TTGTGGCTACTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATCTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CTTCTGCTCTAAAGCTGCG and 3' end primer
CGACCTGCAGCTCGACACA."
BASE COUNT 193 a 124 c 94 g 157 t
ORIGIN

Alignment Scores:
Pred. No.: 8.91e-99 Length: 568
Score: 911.00 Matches: 172
Percent Similarity: 91.79% Conservative: 7
Best Local Similarity: 88.21% Mismatches: 10
Query Match: 45.73% Indels: 6
DB: 9 Gaps: 1

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US-09-944-884-2 (1-379) x AI006670 (1-568)
QY      11 AlaLeuCysSerAlaLysProPheSerHisIleAlaLeuLysAsnMet 30
Db      2 GCTGTGCTCTGCCAAACCTTCTTTAGCCCTTCCACACAGCACTGAAGATATGATG 61
QY      31 LeuLysAspMetGluAspThrAspAspAspAspAspAspAspAspAsp 50
Db      62 TTGAAGGATATGAAGACACAGATGATGACGATAAGCATGATGAC----- 106
QY      51 GluAspAsnSerLeuPheProThrArgGluProArgSerHisPhePheProPheAspLeu 70
Db      107 ---GCAAACTCTCTTTTCCAAAGAGAGCCAGTGAACCTTTTTCCTTTTCGATTG 163
QY      71 PheProMetCysProPheGlyCysGlnCysTyrSerArgValValHisCysSerAspLeu 90
Db      164 TTTCACCATGTCATTTGGTGCCTAATGTACTCTCGAGTCTTCTCACTGCTCTGATCTA 223
QY      91 GlyLeuThrSerValProThrAsnIleProPheAspThrArgMetLeuAspLeuGlnAsn 110
Db      224 GGTCTGACATCGGTTCACAAACATTCCTATTTGATACTCGAATGTTGACCTTCAAAAT 283
QY      111 AsnLysIleLysGluIleLysGluAsnAspPheLysGlyLeuThrSerLeuTyrGlyLeu 130
Db      284 AATAAATCAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAAT 343
QY      131 IleLeuAsnAsnLysLeuThrLysIleHisProLysAlaPheLeuThrThrLysLys 150
Db      344 ATTCTGAACAACAACAGCTAACAAAGATTCACCCAAAACCTTCTTAACCAACAAAGA 403
QY      151 LeuArgGluLeuTyrLeuSerHisAsnGlnLeuSerGluLeuProLeuAsnLeuProLys 170
Db      404 TTGAGAAGGCTATATTATCCCAACCAACTAAGTGAATTCACCTTAATCTTCCACAGA 463
QY      171 SerLeuAlaGluLeuArgIleHisGluAsnLysValLysLysIleGlnLysAspThrPhe 190
Db      464 TCATTAGCAGACTCAGATTCATGATAATAAAGTAAGAGATTCAAAAGGACACGTTTC 523
QY      191 LysGlyMetAsnAlaLeuHisValLeuGluMetSerAlaAsnPro 205
Db      524 AAGGGAATGATGCTTTTACATGTTTGGAAATGAGTTGCAAAACCC 568

RESULT 8
BQ882271
LOCUS   936 bp mRNA linear EST 16-AUG-2002
DEFINITION
AGENCOURT 7982177 Lupski dorsal root ganglion Homo sapiens CDNA
clone IMAGE:6186197 5', mRNA sequence.
ACCESSION
BQ882271
VERSION BQ882271.1 GI:22274279
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 936)
AUTHORS
NTH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13578 row: d column: 06
High quality sequence stop: 637.
Location/Qualifiers
1. 936
/organism="Homo sapiens"
/db_xref="taxon:9606"
FEATURES
source

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/clone="IMAGE:6186197"
/clone.lib="Lupski_dorsal_root_ganglion"
/sex="male"
/tissue.type="dorsal_root_ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
Note: Site 2: Salt; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCTGCTAGTCGAGCGGCGGCGCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies.
BASE COUNT 222 a 309 c 246 g 158 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 2,85e-96 Length: 936
Score: 893.00 Matches: 164
Percent Similarity: 77.66% Conservative: 55
Local Similarity: 58.16% Mismatches: 62
Query Match: 44.83% Indels: 1
DB: 14 Gaps: 0
US-09-944-884-2 (1-379) x BQ882271 (1-936)
QY 95 ValProThrasnileProPheAspThrArgMetLeuAspLeuGlnAsnLysileLys 114
Db 2 GTGCCAAGAGATCTCCCTGACACACCGTGTGGAGCTGCAGAACACGACATCC 61
QY 115 GluileLysGluAsnAspPheLysGlyLeuThrSerLeuTyrglyLeuileLeuAsnAsn 134
Db 62 GAGCTCCGCAAGGATGACTCAAGGCTCTCCAGCACCTCTAGCGCCCTGCTGCTGAAC 121
QY 135 AsnLysLeuThrLysileHisProLysAlaPheLeuThrLysLysLysArgArgLeu 154
Db 122 AACAGATCTCAAGATCCATGAGAAGGCTTACGCCACCTGCGGAGAGTGTTCAGCGGCTCCGG 301
QY 155 TyrLeuSerHisAsnGlnLeuSerGluileProLeuAsnLeuProLysSerLeuAlaGlu 174
Db 182 TACATCTCCAGAACACCTGTGTGAGATCCCGCCACCTACCCAGCTCCCTGCTGGAG 241
QY 175 LeuArgileHisGluAsnLysValLysileGlnLysAspThrPheLysGlyMetAsn 194
Db 242 CTCGCGATCCAGCAACCGCATCCGCAAGGTGCGCAAGGAGTGTTCAGCGGCTCCGG 301
QY 195 AlaLeuHisValLeuGluMetSerAlaAsnProLeuAspAsnGlyileGluProgly 214
Db 302 AACATGAACCTGATCGAGATGGCGGGAACCCACCTGGAGAACAGTGTTCGAGCGGCTCCGG 361
QY 215 AlaPheGluGlyValThrValPheHisileArgileAlaGluAlaLysLeuThrSerVal 234
Db 362 GCCTTCGATGGCTCAAGCTCACTACCTGCGCATCTCAGAGCCCAAGCTGAGTCCGATC 421
QY 235 ProLysGlyLeuProProThrLeuLeuGluLeuHisLeuAspTyrAsnLysileSerThr 254
Db 422 CCCAAAGACCTCCCTGAGACCTGTAATGAACCTCCACCTAGACCACACAAATCCAGGCC 481
QY 255 ValGluLeuGluAspPheLysArgTyrLysGluLeuGlnArgLeuGlyLeuAsnAsn 274
Db 482 ATCGAACCTGGAGGAGCTGCTGCTGCTACTCCAGCTGTACAGGCTGGGCTGAGGCCACAC 541
QY 275 LysileThrAspIleGluAsnGlySerLeuAlaAsnileProArgValArgGluileHis 294
Db 542 CAGATCAGATGATCGAAGACGGAGGAGCTGAGCTCTCCACCTCCGGGAGCTCCAC 601
QY 295 LeuGluAsnAsnLysLysileProSerGlyLeuProGluLeuLysTyrLeuGln 314
Db 602 TTGGACAACAACAACTTGCCAGGAGTGCCTCAGGGCTCCAGGACCTCCAGCTCCTCCAG 661

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QY 315 IlellePheLeuHisSerAsnSerileAlaArgValGlyValAsnAspPheCysProThr 334
Db 662 GTGGTCTATCTGCATCTCCAAACATCACCAGAGGGGTGTCAAGACTTCTGTCCCATG 721
QY 335 ValProLysMetLysSerLeuTyrglySerAlaileSerLeuPheAsnProVal-Ly 354
Db 722 GCGTTCGGGGTGAAGCGGGCTTACTACAAAGGATCAGCCCTCTTCAACACCGGTGCC 781
QY 354 sTyrrTrpGluMetGlnProAlaThrPheArgCysValLeuSerArgMetSerValGlnLe 374
Db 782 CTACTGGGAGTGCAGCGGCGGCTTCCCGTGGCTGCTACTGACCGCGCTGGNCATCCAGTT 841
QY 374 uGly 375
Db 842 TGGG 845
RESULT 9
AL600795 592 bp mRNA linear EST 14-AUG-2001
LOCUS
DEFINITION DKFZp313E0538_r1 313 (synonym: hicc2) Homo sapiens cDNA clone
ACCESSION DKFZp313E0538 5', mRNA sequence.
VERSION AL600795.1 GI:15164301
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 592)
AUTHORS Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
TITLE EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT Contact: Wambutt R
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DKFZp313E0538) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1..592
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/db_xref="taxon:9606"
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/lab_host="DH10B"
/note="Vector: pTriplex2; site_1: SfIIA; site_2: SfiIB;
cDNA-collection"
BASE COUNT 180 a 124 c 110 g 178 t
ORIGIN
Alignment Scores:
Pred. No.: 8,09e-91 Length: 592
Score: 845.00 Matches: 157
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.42% Indels: 0
DB: 9 Gaps: 0
US-09-944-884-2 (1-379) x AL600795 (1-592)
QY 1 MetLysGluTyrValLeuLeuPheLeuAlaLeuCysSerAlaLysProphePheSer 20
Db 121 ATGAGGAGTAGTGTCTCTCTATTTCTGCTGTGCTGCTGCAACCCCTCTTTAGC 180
QY 21 ProSerHisileAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40
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/clone_lib="LTI_FL002_PL1"
/lab_host="PH10B"
/Note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies, Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 255 a 195 c 222 g 315 t 8 others
ORIGIN

```

```

Alignment Scores:
Length: 995
Matches: 149
Conservative: 55
Mismatches: 66
Indels: 1
Gaps: 1
Percent Similarity: 75.28%
Best Local Similarity: 54.98%
Query Match: 40.59%
DB: 9

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US-09-944-884-2 (1-379) x AL568847 (1-995)

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QY 108 LeuGlnAsnAsnLysLysGluLysGluAsnAspPheLysGlyLeuThrSerLeu 127
DB 994 CTCGAAACAAACAAATACCGGAAATCAAGATGAGGACTTTAAGAACCTGACGACCTT 935
QY 128 TyrGlyLeuLeuAsnAsnLysLeuThrLysLysLysLysLysLysLysLysLys 147
DB 934 CACGCAATGATCTTTCACACATAAATAGCAAGATTAGTCTCTGAGGATTACACCT 875
QY 148 ThrLysLysLeuArgLeuThrLeuSerHisAsnGlnLeuSerGluLeuProLeuAsn 167
DB 874 TTGGTGAAGTTGCAAGCACTTTATCTGCTCCAGAAATCAGCTGAAGAAATGCCAGAAAA 815
QY 168 LeuProLysSerLeuAlaGluLeuArgLysLysLysLysLysLysLysLysLys 187
DB 814 ATCCCAAACTCTTCAGGAGCTGCGTGCCCATGAGATGAGATCACCAGAGTCCGAAAA 755
QY 188 AspThrPheLysGlyMetAsnAlaLeuHisValLeuGluMetSerAlaAsnProLeuAsp 207
DB 754 GTTACTTCAATGAGTACGACCATGATGTCATAGAACTGGGACCAATCCGCTGAAG 695
208 AsnAsnGlyLeuProGlyAlaPheGluGlyVal---ThrValPheHisLysLeu 226
DB 694 AGCTCAGGAATGAAAATGGGCTTCCAGGAATGAAGACTCTCTACATCCGCAAT 635
QY 227 AlaGluAlaLysLeuThrSerValProLysGlyLeuProProThrLeuLeuLeuHis 246
DB 634 GGTGATACCAATATCACCAGCATCTCTCAAGGCTTCTCTCCCTACGGAATATACAT 575
QY 247 LeuAspTyrAsnLysLysLysLysLysLysLysLysLysLysLysLysLysLys 266
DB 574 CTGTATGGCAACAAATACAGCAGATTGATGACCTAGCTAGGAGGACTGAATATTG 515
QY 267 GlnArgLeuGlyLeuGlyAsnAsnLysLysLysLysLysLysLysLysLysLys 286
DB 514 GCTAAGTTGGATTGATTCACAGCATCTCTGCTGTTTACCAATGCTCTCTGGCCAAAC 455
QY 287 IleProArgValArgGluLeuHisLeuGluAsnAsnLysLysLysLysLysLysLys 306
DB 454 ACGCCTCATCTGAGGAGCTTCACTTGGACAAACAAGCTTACCAGAGTACCTGGTGGG 395
QY 307 LeuProGluLeuLysLysLysLysLysLysLysLysLysLysLysLysLysLys 326
DB 394 CTGGCAGACATAGTATACAGGTTGCTACCTTCATACCAATATCTCTGTAGTT 335
QY 327 GlyValAsnAspPheCysProThrValProLysMetLysLysLysLysLysLysLys 346
DB 334 GGATCAAGTCACTCTGCCCACTCCGACACACACCAAGAGCTCTTATTCGGGTCTG 275

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QY 347 SerLeuPheAsnAsnProValLysTyrTrpGluMetGlnProAlaThrPheArgCysVal 366
DB 274 AGTCTTTTCAGCAACCCGGTCCAGTACTGGAGATACCCATCCACTTCAGATGTGTC 215
QY 367 LeuSerArgMetSerValGlnLeuGlyAsnPhe 377
DB 214 TACGTCGGCTCTGCCATTCACACTCGGAAACTAT 182
RESULT 13
AL571404/c 879 bp mRNA linear EST 16-FEB-2001
LOCUS LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI023YG19 3
DEFINITION prime, mRNA sequence.
ACCESSION AL571404
VERSION AL571404.1 GI:12928667
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 879)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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1. 879
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/db_xref="taxon:9606"
/clone="CS0DI023YG19"
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/Note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 223 a 179 c 204 g 270 t 3 others
ORIGIN
Alignment Scores:
Pred. No.: 1,11e-85 Length: 879
Score: 804.50 Matches: 149
Percent Similarity: 75.00% Conservative: 55
Best Local Similarity: 54.78% Mismatches: 67
Query Match: 40.39% Indels: 1
DB: 9 Gaps: 1
US-09-944-884-2 (1-379) x AL571404 (1-879)
QY 107 AspLeuGlnAsnAsnLysLysLysLysLysLysLysLysLysLysLysLysLys 126
DB 877 GACCTGCAAAACACAAATACCGAAATCAAGATGAGACTTTAAGAACCTCAAGAAC 818
QY 127 LeuTyrGlyLeuLeuLeuAsnAsnLysLysLysLysLysLysLysLysLysLys 146
DB 817 CTTCAAGCATGATCTTCTGTCACAAATAAATAGCAAGTTAGTCTCTGGAGCATTTACA 758
QY 147 ThrThrLysLysLeuArgLeuThrLeuSerHisAsnGlnLeuSerGluLeuProLeu 166
DB 757 CCTTTGGTGAAGTTGGAACGACTTTATCTTCAAGAAATCAGCTGAGGAATTCAGCA 698
QY 167 AsnLeuProLysSerLeuAlaGluLeuArgLysLysLysLysLysLysLysLys 186
DB 697 AAATGCCAAACTCTTCAGGAGCTCGTCCCATGAGATGAGATCACCAGGTCGGA 638

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Qy 187 LysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGluMetSerAlaAsnProLeu 206
 Db 637 AAGTTACTTTCAATGGACTGAACACAGATGTTGTATAGAACTGGGACCAATCCGCTG 578
 Qy 207 AspAsnGlyIleGluProGlyAlaPheGluGlyVal---ThrValPheHisIleArg 225
 Db 577 AAGAGCTCAGGAATGAAATGGGGCTTCCAGGGAATGAAGAAGCTCTCTACATCCGC 518
 Qy 226 IleAlaGluAlaLysLeuThrSerValProLysGlyLeuProProThrLeuLeuGluLeu 245
 Db 517 ATTGCTGATACCAATATACACAGCATCTCTCAAGGTCTCTCTCTCTCTCTCTCTCT 458
 Qy 246 HisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPheLysArgTyrLysGlu 265
 Db 457 CATCTTGTGATGGCAACAAATACAGACAGATGATGATGATGATGATGATGATGAT 398
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 Qy 306 GlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSerAsnSerIleAlaArg 325
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 ACCESSION AL541759
 VERSION AL541759.1 GI:12873134
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 974)
 AUTHORS Li, W. B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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 /db_xref="taxon:9606"
 /clone_lib="C50DE007YM07"
 /lab_host="DH10B"
 /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
 cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-stranded cDNA was digested with Not I
 and cloned into the Not I and Eco RV sites of the
 pCMVSPORT 6 vector. Library was constructed by Life

Technologies. Contact : Feng Liang Life Technologies, a
 division of Invitrogen 9800 Medical Center Drive Rockville
 Maryland 20850, USA Fax : (1) 301 610 8371 Email :
 fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 284 a 231 c 203 g 248 t 8 others
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Alignment Scores:
 Pred. No.: 1,04e-84 Length: 974
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US-09-944-884-2 (1-379) x AL541759 (1-974)

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 Qy 174 GluLeuArgIleHisGluAsnLysValLysIleGlnLysAspThrPheLysGlyMet 193
 Db 301 GAGCTGCTGCCCTCAGATGAGATGATCACCAGAGTGGCAAAAGTTACTTTCAATGAGCTG 360
 Qy 194 AsnAlaLeuHisValLeuGluMetSerAlaAsnProLeuAspAsnGlyIleGluPro 213
 Db 361 AACAGATGATTTGTCATAGAACTGGGCACCAATCCGCTGAAGAGCTCAGAAATTGAAAT 420
 Qy 214 GlyAlaPheGluGlyVal---ThrValPheHisIleArgIleAlaGluAlaLysLeuThr 232
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 Db 780 CCACCTGGACACACACCAAAAGGCTTCTTATTCGGGTGTGAGT---YTTTCAGCAGCCC 836

QY	353	vallystryrtrpGlumetGlnProAlaThrPheargCysVal 366
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DEFINITION	AGENCOURT_7976210 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214605	
ACCESSION	BQ708510	
VERSION	BQ708510.1	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REMARKS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 955)	
TITLE	NIH-MGC http://mgc.nci.nih.gov/.	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)	
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Dr. Mark Watson cDNA Library Preparation: Rubin Laboratory DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LUCM382 row: c column: 22 High quality sequence start: 6 High quality sequence stop: 663. Location/Qualifiers 1..955 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:6214605" /clone_lib="NIH_MGC_113" /lab_host="DH10B (phage-resistant)" /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr. priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."	
FEATURES		
source		
BASE COUNT	217 a 326 c 258 g 153 t	1 others
ORIGIN		
Alignment Scores:		
Pred. No.:	2.55e-82	Length: 955
Score:	777.00	Matches: 138
Percent Similarity:	79.57%	Conservative: 49
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: May 31, 2003, 10:29:02 ; Search time 6337 Seconds
(without alignments)
11270.047 Million cell updates/sec

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: gb.in : *
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	2454	100.0	2454	6	AX490922	Sequence
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6	1862.8	75.9	1903	9	AK000136	Homo sapi
7	1786.8	72.8	2089	9	AK027359	Homo sapi
8	1254.8	51.1	152341	9	AL137848	Human DNA
9	1184	48.2	1184	9	AF316824	Homo sapi
10	1122.6	45.7	2325	10	BC034888	Mus muscu
11	911	37.1	1165	10	AF316825	Mus muscu
12	462	18.8	496	6	AX210520	Sequence
13	368	15.0	1634	5	AF247821	Oreochrom
14	367.8	15.0	2960	5	AB037269	Xenopus l
15	328.8	13.4	263505	2	AC123954	Mus muscu
16	312	12.7	2446	10	RN017834	Rattus norv
17	310.4	12.6	1107	6	A77048	Sequence 1
18	305.8	12.5	182798	2	AC025394	Homo sapi
19	305.2	12.4	1492	4	AF125537	Sus scrofa
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21	301	12.3	964	4	OC003394	Oryctolagus
22	301	12.3	1553	4	S76584	decorin-pro
23	299.8	12.2	1964	10	MMPGI	X53928 M.musculus
24	299.8	12.2	2372	10	MUSBIGLY	L20276 Mouse bigly
25	299.8	12.2	2383	10	BC005452	Mus muscu
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ALIGNMENTS

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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AX400320
Sequence 1 from Patent EP1191101.
AX400320
AX400320.1 GI:21336501
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Baker,K.P., Chen,J., Goddard,A., Gurney,A.L., Wood,W.I. and Yuan,J.
Polypeptides and nucleic acids encoding the same
Patent: EP 1191101-A 1 27-MAR-2002;
linear PAT 05-JUN-2002

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RESULT 3
AX464194 LOCUS 2454 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 327 from Patent WO0140466.
ACCESSION AX464194
VERSION AX464194.1 GI:218999113
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,
Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Wood, W.L. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
same
JOURNAL Patent: WO 0140466-A 327 07-JUN-2001;
Genentech Inc. (US)
FEATURES
Location/Qualifiers
source 1. 2454
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 835 a 432 c 417 g 770 t
ORIGIN

Query Match 100.0%; Score 2454; DB 6; Length 2454;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS

Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Pooni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.

Compositions and methods for the diagnosis and treatment of

disorders involving angiogenesis
Patent: WO 0200690-A 29 03-JAN-2002;

JOURNAL

Genentech, Inc. (US)

FEATURES

Location/Qualifiers

Source

1. 2454

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/db_xref="taxon:9606"

BASE COUNT 835 a 432 c 417 g 770 t

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RESULT 5
LOCUS AY029191
DEFINITION Homo sapiens periodontal ligament associated protein 1 (PLAP1)
mRNA, complete cds.
VERSION AY029191
KEYWORDS AY029191.1 GI:16151084
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2466)
AUTHORS Yamada,S., Murakami,S., Matoba,R., Ozawa,Y., Yokokoji,T.,
Nakahira,Y., Ikezawa,K., Takayama,S., Matsubara,K. and Okada,H.
TITLE Expression profile of active genes in human periodontal ligament
and isolation of PLAP-1, a novel SLRP family gene
JOURNAL Gene 275 (2), 279-286 (2001)
MEDLINE 21472263
PUBMED 11587855
REFERENCE 2 (bases 1 to 2466)
AUTHORS Yamada,S., Murakami,S., Matoba,R., Matsubara,K. and Okada,H.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2001) Department of Periodontology, Osaka
University Graduate School of Dentistry, 1-8 Yamadaoka, Suita,
Osaka 565-0871, Japan
FEATURES
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RESULT 8
ALI37848/CLOCUS
DEFINITIONACCESSION
VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

ALI37848 152341 bp DNA linear PRI 10-JAN-2002
Human DNA sequence from clone RP11-77D6 on chromosome 9q31.1-32,
complete sequence.

ALI37848
ALI37848.5 GI:18135034
HTG.

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 152341)
Ramsay, H.

Direct Submission
Submitted (10-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk

On Jan 11, 2002 this sequence version replaced gi:930935.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw:
SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP

database can be found at
http://www.sanger.ac.uk/Projects/C-elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human

chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr9

RP11-77D6 is from the library RPCI-11.1 constructed by the group of
Piet de Jong. For further details see
http://www.chori.org/bacpac/home.htm

VECTOR: pBACE3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-77D6 it may be shorter because we sequence overlapping

sections only once, except for a short overlap.
The true right end of clone RP11-77D6 is at 152341 in this
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sequence. The true right end of clone RP11-62C3 is at 2000 in this

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RESULT 9
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DEFINITION AF316824
ACCESSION AF316824
VERSION AF316824.1 GI:13625796
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1184)
AUTHORS Lorenzo,P., Aspegberg,A., Onnerfjord,P., Bayliss,M.T., Neame,P.J. and Heinegard,D.
TITLE Identification and characterization of asporin, a novel member of the leucine-rich repeat protein family closely related to decorin and biglycan
J. Biol. Chem. 276 (15), 12201-12211 (2001)

JOURNAL MEDLINE
PUBMED 21192276
REFERENCE 2 (bases 1 to 1184)
AUTHORS Aspberg,A.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-2000) Cell and Molecular Biology, Lund University, BMC plan C12, Lund SE-221 84, Sweden
FEATURES source
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misc_feature 178..180

QY	996	GTGGAACTTGAGGATTTAAACGATACAAAGGCTGGGCTAGGAACAAC	1055																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		</
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Db 1418 AATACTGGCCATACAGCGGCAACCTTTCGCTGCGTGACCGGACGAGGGGTGTTACG 147

QY 1353 CTTGGGAACCTTTGGAATGTA 1372

Db 1478 CTCGGAACCTTCAGAAAGTA 1497

RESULT 14

AB037269 2960 bp mRNA linear VRT 26-JAN-2000

LOCUS

DEFINITION Xenopus laevis BGN mRNA for biglycan, complete cds.

ACCESSION AB037269

VERSION AB037269.1 GI:6759314

KEYWORDS biglycan.

SOURCE Xenopus laevis cDNA to mRNA.

ORGANISM Xenopus laevis

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus.

AUTHORS 1 (bases 1 to 2960)

TITLE Goto,T. and Kubota,H.Y.

JOURNAL cDNA of biglycan of Xenopus laevis

REFERENCE 2 (bases 1 to 2960)

AUTHORS 2 (bases 1 to 2960)

TITLE Goto,T. and Kubota,H.Y.

JOURNAL Direct Submission

Submitted (20-JAN-2000) Toshiyasu Goto, Graduate School of Science, Kyoto University, Department of Zoology; Sakyo-ku, Kyoto 606-8502, Japan (E-mail:goto@develop.zool.kyoto-u.ac.jp, Tel.:+81-75-753-4082, Fax:+81-75-753-4080)

FEATURES

source Location/Qualifiers.

1..2960

/organism="Xenopus laevis"

/db_xref="taxon:8355"

1..2960

/gene="BGN"

266..1372

/gene="BGN"

/codon_start=1

/product="biglycan"

/protein_id="BAA90246.1"

/db_xref="GI:6759315"

/translation="MKVLLLCSCILVIHALPFEQRFWFDFSMDDGMAMMKDEASGVGPITESIPDVGVPDMLCFPGQCHLRVQCSDLGITSIPKNLPKDTLLDLDQNNKISTEIKDDFGKGLNLYALVIVNNKISKINEKAFLEPQMKQLYISKNLEIEIPKNLKSLEVRLEHNIKKVPKGVFSGLKNMNCIEMGNPLENGGIEAGAFDGLKINLYRVSBAKLSGIPKGLPSTLNLELDNNKIQAIKEKDLVSASLYRLGLGHNNHMTENGSLSEFVPLRELHLDDNKLSKVPGLPDMKLLQVYLHNSNIYQVGVNDPCPIGFVGKRAYYNGISLFNNPVPTWEVQPATFRCVTRDLAIQFGRYRK"

BASE COUNT 859 a 667 c 652 g 782 t

ORIGIN

Query Match 15.0%; Score 367.8; DB 5; Length 2960;

Best Local Similarity 62.4%; Pred. No. 2.5e-58;

Matches 576; Conservative 0; Mismatches 347; Indels 0; Gaps 0;

QY 451 TGTCTCCATTGGATGTGCAGTGCATTACACGAGTTGTACATTCGTACAGATTAGGTTGA 510

Db 450 TATGCCCATTTGGGTGTCATATGTCATTTCGCTGGTGGTGCAGTGCCTCTGATTTGGGTCTCA 509

QY 511 CCTCAGTCCCAACCAACATCCCATTTGATCTCGAATCTTGATCTTCAAAACAATAAAA 570

Db 510 CGTCTATTCCTCCAAAACCTCCGAAAGACACCACTCTCTTGGATCTACAGAACACAAA 569

QY 571 TTAGGAAATCAAGAAATGATTTTAAAGGACACACTTCTATGCTCTGATCTCTGA 630

Db 570 TCACGGAATCAAAAAGGACACTTCAGGGGACTCACCACTGTATGCTTTGGTTATAG 629

QY 631 ACAACAACAAGCTTAACGAAGATTCCACCCAAAGCGCTTCTTAACCAACAAAAGTTGGCAA 690

Db 630 TCACACAACAAGATATCGAAATCAATGAAAGAGCGCTTTGAGCCCTTCGACAGATGAGA 689

QY 691 GGCTGTATCTGTCGCCCAACAACAACTAAGTGAATACCACTTAACTTCCCAAAATCATTAG 750

Qy	1293	AAATACCTGGGAAATGCAACCTGCAACATTTTCGTTGTGTTTGGAGCAGAAATGAGTGTTCAG	1352
Db	131484	AAGTACTGGGAAATACAAACCTGCAACATTTTCGTTGTGTTTGGAGCAGAAATGAGTGTTCAG	131425
Qy	1353	CTTGGGAACTTTGGAAATGTAATAATTAGTAATTTGGTAATGTCCTATTTAATATAAGATTCA	1412
Db	131424	CTTGGGAACTTTGGAAATGTAATAATTAGTAATTTGGTAATGTCCTATTTAATATAAGATTCA	131375
Qy	1413	AAAATCCTACATTTTGGAAATCTTTGAACCTCTATTAAATAGGTAGTATTATATATACAAAG	1472
Db	131374	AAAATGTAACATTTTGGAAATCTTTGAACCTCTATTAAATAGGTAGTATTATATACAAAG	131315
Qy	1473	CAAAATCTATTCTCAAGTGGTAAGTCCACAGCTTATTTTATGACAGAAATTTTCAACG	1532
Db	131314	CAAAATTTCTATTCTT-----ATATGGTCAATGACAAAAATTTCAACA	131273
Qy	1533	GAATTTTGGCAAACTATTGTACATAAGGGGTTGAGAGAAACACGACTATTGCGAGTTT	1592
Db	131272	GAATTTTGGCAAACTATTGTATGATGCTCAG-----ATAAATTTCTATTGCGAGTGT	131225
Qy	1593	CTTTTTCGGGTACAAATGATCTACATAAAATCTCATGCTTGACCAATTCCTTTCTTCATAA	1652
Db	131224	CTTCTGCACATGAATGATCTTCCGTAAATCTTTGCTTGACACATCTCTTTT-----	131171
Qy	1653	CAAAAAAGTAAGATATTTCGGTATTTAACACACTTTGTTATCAAGCACATTTTAAAAAGACT	1712
Db	131170	CGGCAAAAAAGATATTTAGTATTTAACCCCTTCATTATCAAG--TCAGTCAAAACAGAATT	131113
Qy	1713	GTACTGTAAATGGAATGCTTGACCTTAGCAAAATTTTGCTCTTTTCATTTCGTGTTAGAA	1772
Db	131112	GTACTGTAAACAGAAATGCTTGACCTTAGCAATTTTGTG--TCATATCTTTGCTGTTAGAA	131054
Qy	1773	AACAGAATTAACAAGACAGTAATCTGTAAGAGAGTCATTACACATATCTTATTCTTTAGT--	1831
Db	131053	ANCAAACTGCCAAGACAGCAATTTGGAAGAGTACATATATTTTAGTAGTTTTTTTAAAA	130994
Qy	1832	--AACTTGGGTAGTACTGTAATATTTTTTAATCATCTTAAAGTAGATTGTATATATCTTT	1889
Db	130993	AAAACCTTGGACAGTACTGTAATGTTTCCAAATATCTTGAATACATATAGTTTGGAC----	130938
Qy	1890	ATTGAATTAACCTTATCATGCTTTAGAGCCCGCTTTTATGTTTAAACATAATTTCTTAA	1949
Db	130937	-----AGAAATCAAAATTTCTCAACTCATAT	130915
Qy	1950	ATAAGCCCTTCAGTAAATGTTTCATTACCAACTTGTATAAATGCTACTCTCAAGAGCTGGTT	2009
Db	130914	ATAAGCTTCAAGTA-----TTACAGATAATATATCATCAGAGTTGGTT	130871
Qy	2010	TGGGCTATAGCATATGCTTTTTTTTTTAAATATTACCTGATTATAAAATCTCTGTAA	2069
Db	130870	T--GGGCTATAACATGAATATCTTTTTTAAATTTAACTGGCTATAAAATGTTAAAAA	130812
Qy	2070	AAACGCTPAGTGTTCATPAAATCTGTAACCTGCGCATTTTAAATGATCCGCTATTTAAGCT	2129
Db	130811	TATAATGATGCTAATATAAATAATCTATATGTGTCATTTTA--TGATCAGTTATATAAGCT	130754
Qy	2130	TTTAAATACCATGAAAATTTTAGGCTATATACATTTGCCACTTCAACTCTAAGGAATATT	2189
Db	130753	TTGAAGAACACAGTAACCTGTTAGGTTTACATAGTGTATTATCTCAACTAGGAATA----	130698
Qy	2190	TTTGAGATATCCCTTTTGGAAAGACCTTGCTTGGGAAGAGCCCTGGACACATAACAATTTCTAC	2249
Db	130697	TTCAGGATATCCCTTTTGGAACAGTATGAGCGCCA-----ATCAATTTTATAT	130651
Qy	2250	CAAAATTTGCTCTTCAAAATACGTTATGGACTGGGATAAATCTGTAGAAAAACACATCTAGTATAAC	2309
Db	130650	CAACTTATCTCTTCAAAATATGCACATTTGGTAAATGCCGTGAAACATAGCTAAGGTGACAA	130591
Qy	2310	TGAATAACGACAGCATCAAAATTAACAC	2337
Db	130590	AAACTGAAACTGAAACAAACTTAATAG	130563

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2003, 09:47:27 ; Search time 556 Seconds
(without alignments)
9939.575 Million cell updates/sec

Title: US-09-944-884-1

Perfect score: 2454

Sequence: 1 ggaactaatctgtggagcagc.....taaaatattgttgaat 2454

Scoring table: IDENTITY_NUC

Gapex 10.0 , Gapex 1.0

atched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	2454	100.0	2454	20 AAX80043	Human PRO241 nucle
2	2454	100.0	2454	22 AAS21407	Human cDNA sequenc
3	2454	100.0	2454	24 ABL95575	Human angiogenesis
4	2454	100.0	2454	20 ABL88086	Human PRO241 cDNA
5	2443	99.6	2455	21 AAA49551	Human PRO241 cDNA
6	1786.8	72.8	2089	22 AAH18405	Human cDNA sequenc
7	1524	62.1	1674	22 AAS33113	DNA encoding human
8	1427.4	58.2	1548	22 AAS19507	Human polynucleoti
9	1288.8	52.5	1492	23 AAS86756	DNA encoding novel

10	1254.8	51.1	18595	22 AAS33411	DNA encoding human
11	1136.6	46.3	2305	24 ABL10114	Mouse bone/cartila
12	1136.6	46.3	2305	24 ABL35045	Murine cDNA isolat
13	790.2	32.2	896	22 AAI94377	Human neuroblastom
14	785.6	32.0	814	22 AAI61293	Human polynucleoti
15	774.8	31.6	854	22 AAH16847	Human cDNA clone (
16	614	25.0	899	22 AAI94378	Human neuroblastom
17	497	20.3	508	21 AAC00247	Human secreted pro
18	497	20.3	508	21 AAC00247	Human 5' EST isola
19	496.6	20.2	574	21 AAH16901	Human cDNA clone (
20	462	18.8	496	22 AAH1653	Human differential
21	328	13.4	330	20 AAX41488	Human secreted pro
22	312	12.7	2446	16 AAT08768	Rat biglycan cDNA.
23	295.4	12.0	1002	14 AAQ50046	Mature decorin PT-
24	295.4	12.0	1026	17 AAT10741	Human recombinant
25	295.4	12.0	1837	20 AAZ41383	Human normal uteru
26	295.4	12.0	2063	23 ABV22279	Human prostate exp
27	295.4	12.0	2063	23 ABV24765	Human prostate exp
28	295.4	12.0	2063	23 ABV26594	Human prostate exp
29	295.4	12.0	2063	23 ABV28113	Human prostate exp
30	295.4	12.0	2063	23 ABV28779	Human prostate exp
31	295.4	12.0	2078	20 AAZ41275	Human normal ovari
32	295.4	12.0	2119	23 ABK43616	DNA encoding novel
33	295.4	12.0	4167	21 AAA12499	cDNA encoding a ch
34	295.4	12.0	4192	17 AAT16517	Collagen A1/decori
35	294.6	12.0	1685	22 AAD07372	Human DNA encoding
36	294.6	12.0	1685	22 AAF83977	Human biglycan enc
37	294.6	12.0	1685	24 ABL62863	Breast cancer rela
38	294.6	12.0	1685	24 ABL63084	Breast cancer rela
39	294.6	12.0	1685	24 ABL64383	Stomach cancer rel
40	294.6	12.0	2296	24 ABK35121	Human cDNA encodin
41	294.6	12.0	2367	20 AAZ53010	Human prostate tum
42	294.6	12.0	2384	20 AAZ24428	Human bladder tumo
43	294.6	12.0	6321	11 AAS94760	Human DNA sequenc
44	291.4	11.9	1685	24 AAQ04490	Sequence encoding
45	283.8	11.6	591	23 ABV58751	Human prostate exp

ALIGNMENTS

RESULT 1

AAX80043
ID AAX80043 standard; cDNA; 2454 BP.

AC AAX80043;

XX 12-AUG-1999 (first entry)

XX Human PRO241 nucleotide sequence.

DE Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
secreted protein; transmembrane protein; inflammation disorder; ss.

XX Homo sapiens.

XX WO9928462-A2.

XX 10-JUN-1999.

XX 01-DEC-1998; 98WO-US25108.

XX 25-FEB-1998; 98US-0075945.

XX 03-DEC-1997; 97US-0067411.

XX 11-DEC-1997; 97US-0069278.

XX 11-DEC-1997; 97US-0069334.

XX 11-DEC-1997; 97US-0069335.

XX 12-DEC-1997; 97US-0069425.

XX 16-DEC-1997; 97US-0069694.

XX 16-DEC-1997; 97US-0069696.

XX 17-DEC-1997; 97US-0069702.

XX 17-DEC-1997; 97US-0069870.

XX 17-DEC-1997; 97US-0069873.

PR 18-DEC-1997; 97US-0068017.
PR 05-JAN-1998; 98US-0070440.
PR 09-FEB-1998; 98US-0074086.
PR 09-FEB-1998; 98US-0074092.
XX (GETH) GENENTECH INC.
PA
XX PI Baker KP, Chen J, Goddard A, Gurney AL, Wood WI;
PI Yuan J;
XX
XX WPI: 1999-371118/31.
DR P-PSDB; AAY17820.
XX
XX Nucleic acids encoding PRO secreted and transmembrane proteins
XX
XX Claim 2; Fig 1; 123pp; English.
XX
CC The present invention describes nucleic acids encoding PRO secreted and
CC transmembrane proteins used therapeutically. The PRO proteins have
CC cytosolic, anti-inflammatory, anti-proliferative and immunosuppressive
CC activity. The proteins and polynucleotides can be used in therapy.
CC identification of homologues, raising antibodies and design of probes
CC and primers. They can be used in a range of diseases related to proteins
CC that they have homology with, e.g. a PRO protein having homology to
XX complement proteins may be used in inflammatory responses.
XX
SQ Sequence 2454 BP; 835 A; 432 C; 417 G; 770 T; 0 other;
Query Match 100.0%; Score 2454; DB 20; Length 2454;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGACTAATCTGGGAGCAGTTTATCCAGTATCACCCAGGGTGCAGCCACACAGGACT 60
Db 1 GGACTAATCTGGGAGCAGTTTATCCAGTATCACCCAGGGTGCAGCCACACAGGACT 60
Qy 61 GTGTTGAAGGGTGTCTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTCTTACAC 120
Db 61 GTGTTGAAGGGTGTCTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTCTTACAC 120
Qy 121 AGTCTCTGAGACATTTACATATTAGATAAGTAGATGATGGTGATCTTCTACTTTTA 180
Db 121 AGTCTCTGAGAACATTTACATATTAGATAAGTAGATGATGGTGATCTTCTACTTTTA 180
Qy 181 GGAGACTACTCTCTCGACAGTCCTAGACTGTCTTCTACATAAGACACCATGAAGG 240
Db 181 GGAGACTACTCTCTCGACAGTCCTAGACTGTCTTCTACATAAGACACCATGAAGG 240
Qy 241 AGTATGTCTCTTATTTATTCCTGGCTTGTGCTCTGCGCAACCCCTCTTTAGCCCTTAC 300
Db 241 AGTATGTCTCTTATTTATTCCTGGCTTGTGCTCTGCGCAACCCCTCTTTAGCCCTTAC 300
Qy 301 ACATCGCACTGAAGAATATGATGCTGAAGNATGGAAGACACAGATGATGATGATG 360
Db 301 ACATCGCACTGAAGAATATGATGCTGAAGNATGGAAGACACAGATGATGATGATG 360
Qy 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Db 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Qy 421 GCCATTTTTTCCATTTGATCTGTTTCCCAATGTGCTCCATTTGGATGTCAGTCTATTTCAC 480
Db 421 GCCATTTTTTCCATTTGATCTGTTTCCCAATGTGCTCCATTTGGATGTCAGTCTATTTCAC 480
Qy 481 GAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
Db 481 GAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
Qy 541 CTCGAATGCTGATCTTCAAAACATTAATTAAGGAATCAAGAAATGATTTTAAAG 600
Db 541 CTCGAATGCTGATCTTCAAAACATTAATTAAGGAATCAAGAAATGATTTTAAAG 600
Qy 601 GACTCACTTCTATGGTCTGATCCTGTAACAACAACAGCTTAACGAAGATTCACCCAA 660

Db 601 GACTCACTTCTATGGTCTGATCCTGAACAACAACAGCTTAACGAAGATTCACCCAA 660
Qy 661 AAGCCTTTCTAACCAACAAGAAGTTGCGAAGGCTGTATCTGTCCCAACAATCACTAAGTG 720
Db 661 AAGCCTTTCTAACCAACAAGAAGTTGCGAAGGCTGTATCTGTCCCAACAATCACTAAGTG 720
Qy 721 AAATACCACCTTAATCTTCCCAAAATCATTAGCAGAACTCAGAAATTCATGAAATAAAGTTA 780
Db 721 AAATACCACCTTAATCTTCCCAAAATCATTAGCAGAACTCAGAAATTCATGAAATAAAGTTA 780
Qy 781 AGAAATACAAAAGGACACATTCAAAAGGAATGAATGCTTTTACACGTTTGGAAATGAGTG 840
Db 781 AGAAATACAAAAGGACACATTCAAAAGGAATGAATGCTTTTACACGTTTGGAAATGAGTG 840
Qy 841 CAACCCCTCTTGATAATTAATGGGATAGAGCCAGGGGCATTTGAAGGGTGACGGTGTTC 900
Db 841 CAACCCCTCTTGATAATTAATGGGATAGAGCCAGGGGCATTTGAAGGGTGACGGTGTTC 900
Qy 901 ATATCAGAATTGCGAAGCAAAAACCTGACCTCAGTTCTTAAAGGCTTACCACCAACTTTAT 960
Db 901 ATATCAGAATTGCGAAGCAAAAACCTGACCTCAGTTCTTAAAGGCTTACCACCAACTTTAT 960
Qy 961 TGGAGCTTCACTTAGATTATAATAAATTTCAACAGTGGAACTTTGAGGATTTTAAACGAT 1020
Db 961 TGGAGCTTCACTTAGATTATAATAAATTTCAACAGTGGAACTTTGAGGATTTTAAACGAT 1020
Qy 1021 ACAAGAAGCTTACAAAAGGCTGGCCTAGGAACACAAACATCACAGATATCGAAATGGGA 1080
Db 1021 ACAAGAAGCTTACAAAAGGCTGGCCTAGGAACACAAACATCACAGATATCGAAATGGGA 1080
Qy 1081 GTCTTGCTACATACACACGCTGTGAGAGAAATACATTTTGGAAACAATAAACTTAAAAAAA 1140
Db 1081 GTCTTGCTACATACACACGCTGTGAGAGAAATACATTTTGGAAACAATAAACTTAAAAAAA 1140
Qy 1141 TCCTCTCAGGATTACACAGAGTTGAAATACCTCCAGATAATCTTCTCTCATTTCTAATCAA 1200
Db 1141 TCCTCTCAGGATTACACAGAGTTGAAATACCTCCAGATAATCTTCTCTCATTTCTAATCAA 1200
Qy 1201 TTCCAGAGTGGGAGTAAATGACTTCTTCCACAGTGGCCAAAGATGAAGAAATCTTTAT 1260
Db 1201 TTCCAGAGTGGGAGTAAATGACTTCTTCCACAGTGGCCAAAGATGAAGAAATCTTTAT 1260
Qy 1261 ACAGTGCATTAAGTTTATTTCAACAACCCGGTGAATACTTGGAAATGCAACTGCAACAT 1320
Db 1261 ACAGTGCATTAAGTTTATTTCAACAACCCGGTGAATACTTGGAAATGCAACTGCAACAT 1320
Qy 1321 TTCCTGTGTTTGGAGCAGAAATGAGTGTTCAGCTTGGGAACTTTGGAAATGTAATAATTAG 1380
Db 1321 TTCCTGTGTTTGGAGCAGAAATGAGTGTTCAGCTTGGGAACTTTGGAAATGTAATAATTAG 1380
Qy 1381 TAATTTGTAATGTCCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1440
Db 1381 TAATTTGTAATGTCCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1440
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Db 1441 TCTATTAAATAGTACTATTATATATACAAAGCAAAATATCTTCTCAAGTGGTAAGTCC 1500
Qy 1501 ACTGACTTATTTTATGACAAAGAAATTTCAACGGAAATTTTCCAAACATTTGATACATAAG 1560
Db 1501 ACTGACTTATTTTATGACAAAGAAATTTCAACGGAAATTTTCCAAACATTTGATACATAAG 1560
Qy 1561 GGGTTGAGAGAAACACAGCATCTATTGTCAGTTTCTTTTGGTGGTACAATGATCTTACATA 1620
Db 1561 GGGTTGAGAGAAACACAGCATCTATTGTCAGTTTCTTTTGGTGGTACAATGATCTTACATA 1620
Qy 1621 AATCTCATGCTTGACCATCTCTTTCTTCAATAAACAAGTAAGATATTCGGTATTTTAAAC 1680
Db 1621 AATCTCATGCTTGACCATCTCTTTCTTCAATAAACAAGTAAGATATTCGGTATTTTAAAC 1680
Qy 1681 ACTTTGTTATCAAGACACATTTTAAAGAAAGTGTACTGTAAATGGAATGCTTGACTTAGC 1740
Db 1681 ACTTTGTTATCAAGACACATTTTAAAGAAAGTGTACTGTAAATGGAATGCTTGACTTAGC 1740

1681	Db	ACTTTGTTATCAAGCACATTTTAAAAAGAAC*GTGACTGTAAAT*GGAATGCTTGACTTACG	1740
1741	QY	AAAAATTTGGCTCTTTTCATTCTGTTAGAAAAACAGAAATTAACAAAAGACAGATAATGTGA	1800
1741	Db	AAAAATTTGGCTCTTTTCATTCTGTTAGAAAAACAGAAATTAACAAAAGACAGATAATGTGA	1800
1801	QY	AGAGTGCATTACACATATCTTATCTTTAGTAACTTGGGTAGTACTGTAATATTTTAAAT	1860
1801	Db	AGAGTGCATTACACTATCTTATCTTTAGTAACTTGGGTAGTACTGTAATATTTTAAAT	1860
1861	QY	CATCTTAAAGTATGATTGATATATCTTATTTGAAAT*PACCTATCATCTGCTTAGAGCCC	1920
1861	Db	CATCTTAAAGTATGATTGATATATCTTATTTGAAAT*PACCTATCATCTGCTTAGAGCCC	1920
1921	QY	GTCTTTATCTTTAAAACTAAATTTCTTAAAT*AAAGCCTTCAGTAAATGTTTCATTACCAAC	1980
1921	Db	GTCTTTATCTTTAAAACTAAATTTCTTAAAT*AAAGCCTTCAGTAAATGTTTCATTACCAAC	1980
1981	Db	TTGATAAAT*GCTACTCATAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTTA	2040
1981	Db	TTGATAAAT*GCTACTCATAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTTA	2040
2041	QY	ATTATTTACCTGATTTAAAAATCTCTGTGTAAAAACGTGTAGTGTTCAT*AAAACTGTAACT	2100
2041	Db	ATTATTTACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTCAT*AAAACTGTAACT	2100
2101	QY	CGCATTTTAAATGATCGCTATTATTAAGCTTTTAAATAGCATGAAAT*GTTTAGCTATATA	2160
2101	Db	CGCATTTTAAATGATCGCTATTATTAAGCTTTTAAATAGCATGAAAT*GTTTAGCTATATA	2160
2161	QY	ACATTTGCCACTTCAACTCTAAGGAATATTTTTGAGATATCCCTTTGGAAGACCTTGCCTTG	2220
2161	Db	ACATTTGCCACTTCAACTCTAAGGAATATTTTTGAGATATCCCTTTGGAAGACCTTGCCTTG	2220
2221	QY	GAAGAGCCTGGACACTAACAAATCTACACAAAT*TTCTCTTCAAATAGCTATGGACTGG	2280
2221	Db	GAAGAGCCTGGACACTAACAAAT*TTCTCTTCAAATAGCTATGGACTGG	2280
2281	QY	ATAA*CTCTGAGAAACACATCTAGTATTAACCTGGAATAAGCAGAGCATCAAAATTAACACAGACA	2340
2281	Db	ATAA*CTCTGAGAAACACATCTAGTATTAACCTGGAATAAGCAGAGCATCAAAATTAACACAGACA	2340
2341	QY	GAAAACCGAAGCTCTATATAAAT*GCTCAGAGTTCTTTATGCTATTTCTTATTTGGCATTCAA	2400
2341	Db	GAAAACCGAAGCTCTATATAAAT*GCTCAGAGTTCTTTATGCTATTTCTTATTTGGCATTCAA	2400
2401	QY	CATATCTGAAATCAGAAAAACAGGGAATTTTTCATTTAAAAATAT*TTGTTTGAAT	2454
2401	Db	CATATCTGAAATCAGAAAAACAGGGAATTTTTCATTTAAAAATAT*TTGTTTGAAT	2454

RESULT 2

[illegible]

XX	01-DEC-1999;	99NWO-US28301.
PR	01-DEC-1999;	99NWO-US28634.
PR	02-DEC-1999;	99NWO-US28551.
PR	02-DEC-1999;	99NWO-US28564.
PR	02-DEC-1999;	99NWO-US28565.
PR	09-DEC-1999;	99NWO-US10262.
PR	16-DEC-1999;	99NWO-US20095.
PR	20-DEC-1999;	99NWO-US30911.
PR	20-DEC-1999;	99NWO-US30999.
PR	20-DEC-1999;	99NWO-US31243.
PR	06-JAN-2000;	2000NWO-US20277.
PR	06-JAN-2000;	2000NWO-US00376.
PR	11-FEB-2000;	2000NWO-US03565.
PR	18-FEB-2000;	2000NWO-US04341.
PR	18-FEB-2000;	2000NWO-US04342.
PR	22-FEB-2000;	2000NWO-US04414.
PR	24-FEB-2000;	2000NWO-US04914.
PR	24-FEB-2000;	2000NWO-US05004.
PR	01-MAR-2000;	2000NWO-US05601.
PR	20-MAR-2000;	2000NWO-US07377.
PR	21-MAR-2000;	2000NWO-US07532.
PR	30-MAR-2000;	2000NWO-US08439.
PR	17-MAY-2000;	2000NWO-US13705.
PR	22-MAY-2000;	2000NWO-US14042.
PR	30-MAY-2000;	2000NWO-US14941.
PR	02-JUN-2000;	2000NWO-US52664.
PR	10-NOV-2000;	2000NWO-US30873.

(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W; Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI: 2001-408281/43.

P-PSDB: AAU12335.

Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical -

Claim 3: Fig. 327; 813pp; English.

AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor- α (TNF- α) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake in skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIa. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.

Sequence 2454 BP; 835 A; 432 C; 417 G; 770 T; 0 other;

Query Match 100.0%; Score 2454; DB 22; Length 2454;

Query Match	100.0%;	Score 2434;
Best Local Similarity	100.0%;	Pred. No. 0

Best local similarity	100.00%	100.00%	100.00%	100.00%
Matches 2454;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	

1 GGACTAATCTGTGGGAGCAGTTATTCCAGTATCACCCAGGGTGACCCACACGAGCT 60

|||||
1 GGACAAATCTGGGAGCAGTTTATCCAGTATCACCCAGGTGCGCCACACCGAGCT 60
61 GTGTTGAAGGGTGTCTTTCTTTTAAATGTAATACCTCCTCACTCTTTCTCTTACAC 120
61 GTGTTGAAGGGTGTCTTTCTTTTAAATGTAATACCTCCTCACTCTTTCTCTTACAC 120
121 AGTGTCTGAGAACATTTACATATATAGATAAGTAGTACATGGTGGATAACTTCTACTTTTA 180
121 AGTGTCTGAGAACATTTACATATATAGATAAGTAGTACATGGTGGATAACTTCTACTTTTA 180
181 GGAGGACTACTCTCTCTGACAGTCTTAGACAGTCTTAGACAGTCTCTCTACACATGATGATG 240
181 GGAGGACTACTCTCTCTGACAGTCTTAGACAGTCTTAGACAGTCTCTCTACACATGATGATG 240
241 AGTATGTGCTCTATTTATCTCTGGCTTTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
241 AGTATGTGCTCTATTTATCTCTGGCTTTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
301 ACATCGCACTGAAGATATGATGCTGAAGGATATGAAGACACAGATGATGATGATGATG 360
301 ACATCGCACTGAAGATATGATGCTGAAGGATATGAAGACACAGATGATGATGATGATG 360
361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
421 GCCATTTTTCATTTGATCTGTTTCCAAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
421 GCCATTTTTCATTTGATCTGTTTCCAAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
481 GAGTGTACATTTGCTCAGATTTAGGTTTGCACCTCAGTCCCAACCAACATTTCCATTTGATA 540
481 GAGTGTACATTTGCTCAGATTTAGGTTTGCACCTCAGTCCCAACCAACATTTCCATTTGATA 540
541 CTCGAATGCTTGATCTTCAAAACAATTTAAAGAAATCAAGAAATCAAGAAATCAAGAAATCA 600
541 CTCGAATGCTTGATCTTCAAAACAATTTAAAGAAATCAAGAAATCAAGAAATCAAGAAATCA 600
601 GACTCACTTCACTTTATGCTCTGATCTTCAACCAACCAACCAACCAACCAACCAACCAAC 660
601 GACTCACTTCACTTTATGCTCTGATCTTCAACCAACCAACCAACCAACCAACCAACCAAC 660
661 AAGCCCTTTCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 720
661 AAGCCCTTTCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 720
721 AAATACCACTTAACTTTCCCAATCATTTAGCAGAACTCAGAACTCAGAACTCAGAACTCAG 780
721 AAATACCACTTAACTTTCCCAATCATTTAGCAGAACTCAGAACTCAGAACTCAGAACTCAG 780
781 AGAAATACAAAGGACACATTTCAAGGAATGAATGCTTTACAGCTTTTGGAAATGAGTG 840
781 AGAAATACAAAGGACACATTTCAAGGAATGAATGCTTTACAGCTTTTGGAAATGAGTG 840
841 CAAACCCCTTGTATATAATGGATAGAGCCAGGGGCATTTGAAGGGGTGACGGGTGCTTC 900
841 CAAACCCCTTGTATATAATGGATAGAGCCAGGGGCATTTGAAGGGGTGACGGGTGCTTC 900
901 ATATCAGAAATTCGAGAACCAAACTGACCTCAGTCTTAAAGGCTTTACCACCAACTTTAT 960
901 ATATCAGAAATTCGAGAACCAAACTGACCTCAGTCTTAAAGGCTTTACCACCAACTTTAT 960
961 TGGAGCTTCACTTTAGATTTAATAAATTTCAACAGTGGAACTTTGAGGATTTTAAACGAT 1020
961 TGGAGCTTCACTTTAGATTTAATAAATTTCAACAGTGGAACTTTGAGGATTTTAAACGAT 1020
1021 ACAAGAACTACAAAGGCTTGGGCTTAGGAAACCAACCAACCAACCAACCAACCAACCAAC 1080
1021 ACAAGAACTACAAAGGCTTGGGCTTAGGAAACCAACCAACCAACCAACCAACCAACCAAC 1080
1081 GTCTTCTAACATFACACAGTGTGAGAGAAATACATTTGGAAACCAATAACTAAAAAAA 1140
|||||

Db
1081 GTCTTCTAACATFACACAGTGTGAGAGAAATACATTTGGAAACCAATAACTAAAAAAA 1140
QY
1141 TCCCTTTCAGATTTACAGAGTTGAATACCTCCAGATATCTTCCCTTCTTCTTCTTCTTCTT 1200
Db
1141 TCCCTTTCAGATTTACAGAGTTGAATACCTCCAGATATCTTCCCTTCTTCTTCTTCTTCTT 1200
QY
1201 TTTCAAGAGTGGGAGTAAATGACTTCTGTCCAAACAGTGCACCAAGATGAAGAAATCTTTAT 1260
Db
1201 TTTCAAGAGTGGGAGTAAATGACTTCTGTCCAAACAGTGCACCAAGATGAAGAAATCTTTAT 1260
QY
1261 ACAGTGCATATAGTTTATTCACACACCCGGTGAATACTTGGGAAATGCAACCTGCAACAT 1320
Db
1261 ACAGTGCATATAGTTTATTCACACACCCGGTGAATACTTGGGAAATGCAACCTGCAACAT 1320
QY
1321 TTTGGTGTGTTTGGACAGAAATGAGTGTGCTTGGGAACTTTGGAAATGTAATAATTAG 1380
Db
1321 TTTGGTGTGTTTGGACAGAAATGAGTGTGCTTGGGAACTTTGGAAATGTAATAATTAG 1380
QY
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Db
1381 TAAATGGAATGTCATTTAATAAGATTTCAAAAACTCCCTACATTTGGAATCTTTGAAC 1440
QY
1441 TCTATTAATAAGTGTAGTATTTATATACAGCAATATCTATTTCTCAAGTGGTAAGTCC 1500
Db
1441 TCTATTAATAAGTGTAGTATTTATATACAGCAATATCTATTTCTCAAGTGGTAAGTCC 1500
QY
1501 ACTGACTTATTTTATGACAGAAATTTCAACGGAATTTGCGGTACAAATGATCTTACATA 1560
Db
1501 ACTGACTTATTTTATGACAGAAATTTCAACGGAATTTGCGGTACAAATGATCTTACATA 1560
QY
1561 GGGTTGAGAGAAACAAGCATCTATTGACGTTTCTTTTTCGCTTACAAATGATCTTACATA 1620
Db
1561 GGGTTGAGAGAAACAAGCATCTATTGACGTTTCTTTTTCGCTTACAAATGATCTTACATA 1620
QY
1621 AATCTCATGCTTGACCATCTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1680
Db
1621 AATCTCATGCTTGACCATCTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1680
QY
1681 ACTTTGTTATACAGCACTTTTAAAGAACTGCTACTGTAATGGAATGCTTACACTAGC 1740
Db
1681 ACTTTGTTATACAGCACTTTTAAAGAACTGCTACTGTAATGGAATGCTTACACTAGC 1740
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1741 AAAATTTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1800
Db
1741 AAAATTTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1800
QY
1801 AGAGTGCAATTTACACTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1860
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1801 AGAGTGCAATTTACACTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1860
QY
1861 CATCTTAAAGTATGATTTGATATAATCTTATTCGAAATTTACCTTATCATGCTTAGAGCCC 1920
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1861 CATCTTAAAGTATGATTTGATATAATCTTATTCGAAATTTACCTTATCATGCTTAGAGCCC 1920
QY
1921 GTCTTTATGTTTAAAACTAAATTTCTTAAAAAAGCCTTCAGTAAATGTTTCATTACCAAC 1980
Db
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QY
1981 TTTGATAAATGCTACTCATAGAGCTGTTTGGGGCTTATAGCATATGCTTTTTTTTTTTT 2040
Db
1981 TTTGATAAATGCTACTCATAGAGCTGTTTGGGGCTTATAGCATATGCTTTTTTTTTTTT 2040
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2041 ATTATTTACCTGATTTAAAAATCTCTGTAAGAGCTGATGTTTTCATATAAACTGTAAC 2100
Db
2041 ATTATTTACCTGATTTAAAAATCTCTGTAAGAGCTGATGTTTTCATATAAACTGTAAC 2100
QY
2101 CGCATTTTAAATGATCGCTATTTAAAGCTTTTAAATAGCATGAAATTTGTTAGGCTATATA 2160
Db
2101 CGCATTTTAAATGATCGCTATTTAAAGCTTTTAAATAGCATGAAATTTGTTAGGCTATATA 2160
QY
2161 ACATTTGCCACTTCAACTTAAGGAATATTTTGGAGATATCCCTTTGGAGAGCTTCTGTTG 2220
Db
2161 ACATTTGCCACTTCAACTTAAGGAATATTTTGGAGATATCCCTTTGGAGAGCTTCTGTTG 2220

301 ACATCCGACTGAAGATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATG 360
361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
421 GCCATTTTTCATTTGATGCTCTTCCAAATTAAGGAAATCAAGAAATGATTTTAAAG 480
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601 GACTCACTTCACTTTATGCTGATCCTGAACAACACAGCTTAAGAAATGATTTTAAAG 660
601 GACTCACTTCACTTTATGCTGATCCTGAACAACACAGCTTAAGAAATGATTTTAAAG 660
661 AGCCCTTTTCAACCAAGAAAGTTCGGAAGGCTGATCTGCTCCCAACATCAACTAAGTG 720
661 AGCCCTTTTCAACCAAGAAAGTTCGGAAGGCTGATCTGCTCCCAACATCAACTAAGTG 720
721 AAATACCACTTAATCTTCCCAATCATTAAGGAAATCAAGAAATGATTTTAAAG 780
721 AAATACCACTTAATCTTCCCAATCATTAAGGAAATCAAGAAATGATTTTAAAG 780
781 AGAAATACAAAGGACACATTCAGGAAATGATTTTAAAG 840
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841 CAAACCTCTTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
841 CAAACCTCTTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
901 ATATCAGAAATGAGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 960
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961 TGGAGCTTCACTTATGATTAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1020
961 TGGAGCTTCACTTATGATTAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1020
1021 ACAGAACTACAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1080
1021 ACAGAACTACAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1080
1081 GTCTTCTTACATACCACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1140
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1141 TCCCTTTCAGATTTACAGATTTGAAATACCTCCAGATTAATCTTCCCTTCAATTTCAA 1200
1141 TCCCTTTCAGATTTACAGATTTGAAATACCTCCAGATTAATCTTCCCTTCAATTTCAA 1200
1201 TTGCAAGCTGGAGTAAATGATCTTCCCAACAGCTGCAAGATGAGAAATCTTTAT 1260
1201 TTGCAAGCTGGAGTAAATGATCTTCCCAACAGCTGCAAGATGAGAAATCTTTAT 1260
1261 ACAGTGCATTAAGTTTATTAACCAACCCGCTGAAATACCTGGAAATGCAACCTGCAACAT 1320
1261 ACAGTGCATTAAGTTTATTAACCAACCCGCTGAAATACCTGGAAATGCAACCTGCAACAT 1320
1321 TTCGTTGCTTTTGGAGCAGAAATGAGGTTTCACTTGGGAACTTTGGAATGTAATTAAG 1380
1321 TTCGTTGCTTTTGGAGCAGAAATGAGGTTTCACTTGGGAACTTTGGAATGTAATTAAG 1380
1381 TAATGCTGAATGCTCAATTTAATATAGATTCAGAAATCCCTACATTTGGAATACCTTGAAC 1440
1381 TAATGCTGAATGCTCAATTTAATATAGATTCAGAAATCCCTACATTTGGAATACCTTGAAC 1440

RESULT 4
ABL88086
ID ABL88086 standard; cDNA; 2454 BP.

1441 TCTATTAATAATGCTAGTATTATATACAGCAAAATATCTATTCTCAAGTGTGTAAGTCC 1500
1441 TCTATTAATAATGCTAGTATTATATACAGCAAAATATCTATTCTCAAGTGTGTAAGTCC 1500
1501 ACTGACTTATTTTATGACAGAAATTTCAACGGAATTTTCCCAAACTATTGATACATAAG 1560
1501 ACTGACTTATTTTATGACAGAAATTTCAACGGAATTTTCCCAAACTATTGATACATAAG 1560
1561 GGGTTGAGAGAAACAGCATCTATTGCGAGTTTCCCTTTTCCGCTACAAATGATCTTACATA 1620
1561 GGGTTGAGAGAAACAGCATCTATTGCGAGTTTCCCTTTTCCGCTACAAATGATCTTACATA 1620
1621 AATCTCATGCTTCCACCATTTCTTCTTCAACAAAAAGTAAGATATTGCGTATTAAAC 1680
1621 AATCTCATGCTTCCACCATTTCTTCTTCAACAAAAAGTAAGATATTGCGTATTAAAC 1680
1681 ACTTTGTTATCAAGCACTTTTAAAGAACTGCTACTGTAATGGAATGCTTGCATTTAGC 1740
1681 ACTTTGTTATCAAGCACTTTTAAAGAACTGCTACTGTAATGGAATGCTTGCATTTAGC 1740
1741 AAAATTTGCTCTCTTTTCATTTGCTGTAGAAAAACAGAAATTAACAAAGACAGTAATGTA 1800
1741 AAAATTTGCTCTCTTTTCATTTGCTGTAGAAAAACAGAAATTAACAAAGACAGTAATGTA 1800
1801 AGAGTGCAATTACACTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1860
1801 AGAGTGCAATTACACTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1860
1861 CATCTTAAAGTATGATTTGATATAATCTTATTTGAAATTTACCTTTATCATGCTTTAGAGCCC 1920
1861 CATCTTAAAGTATGATTTGATATAATCTTATTTGAAATTTACCTTTATCATGCTTTAGAGCCC 1920
1921 GTCCTTATGTTTAAAGCACTTAATTTCTTAAATAAAGCTTCAGTAAATGTTTCAATACCAAC 1980
1921 GTCCTTATGTTTAAAGCACTTAATTTCTTAAATAAAGCTTCAGTAAATGTTTCAATACCAAC 1980
1981 TTGATAAATGCTACTCATAGAGCTGTTTGGGGCTATAGCATATGCTTTTCTTTTCTTTT 2040
1981 TTGATAAATGCTACTCATAGAGCTGTTTGGGGCTATAGCATATGCTTTTCTTTTCTTTT 2040
2041 ATTATTACCTGATTTTAAAAATCTCTGTAACAACTGCTAGTGTCTTCAATAAATCTGTAAC 2100
2041 ATTATTACCTGATTTTAAAAATCTCTGTAACAACTGCTAGTGTCTTCAATAAATCTGTAAC 2100
2101 CGCATTTTAAAGTATGATTTTAAAGCTTTTAAATGAGCTTTTAAATGAGCTTTTAAAGCT 2160
2101 CGCATTTTAAAGTATGATTTTAAAGCTTTTAAATGAGCTTTTAAATGAGCTTTTAAAGCT 2160
2161 ACATTTGCCACTTCAACTCTAAGGAATTTTTCAGATATATCCCTTTTGGAGAGCTTCTGTTG 2220
2161 ACATTTGCCACTTCAACTCTAAGGAATTTTTCAGATATATCCCTTTTGGAGAGCTTCTGTTG 2220
2221 GAAGAGCTTGGACACTTAACAAATTTCTACCAAAATTTCTCTTCAAAATACGTATGGACTGG 2280
2221 GAAGAGCTTGGACACTTAACAAATTTCTACCAAAATTTCTCTTCAAAATACGTATGGACTGG 2280
2281 ATAACCTCTGAGAAACACATCTAGTATACTGAATAGAGAGCATCAAAATTAACAGACA 2340
2281 ATAACCTCTGAGAAACACATCTAGTATACTGAATAGAGAGCATCAAAATTAACAGACA 2340
2341 GAAACCGAAGCTCTATATAAATGCTCAGAGTTCTTTATGATTTCTTATTTGCGATTTCAA 2400
2341 GAAACCGAAGCTCTATATAAATGCTCAGAGTTCTTTATGATTTCTTATTTGCGATTTCAA 2400
2401 CATATGTAATAATCAGAAAAACAGGAAATTTTTCATTTAAAAATATTTGTTTGAAT 2454
2401 CATATGTAATAATCAGAAAAACAGGAAATTTTTCATTTAAAAATATTTGTTTGAAT 2454

XX ABL88086;
AC
XX 16-MAY-2002 (first entry)
DT
XX Human PRO241 cDNA sequence SEQ ID NO:29.
DE
XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping; gene; ss.
XX
XX Homo sapiens.
XX WO200200690-A2.
PD 03-JAN-2002.
XX
XX 20-JUN-2001; 2001WO-US19692.
XX
XX 23-JUN-2000; 2000US-213637P.
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 14-MAR-2001; 2001US-0802706.
PR 22-MAR-2001; 2001US-0816744.
PR 03-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001US-0866034.
PR 30-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 01-JUN-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
XX (GETH). GENENTECH INC.
XX Baker KP, Ferrara N, Gerber H, Gerritsen MB, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI: 2002-090516/12.
DR P-PSDB; ABB84831.
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal -
XX

PS
XX
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal.
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC degeneration, atherosclerosis, hypertension, arterial restenosis,
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC carcinoma) and wound healing. The PRO polynucleotides have applications
CC in molecular biology, including use as hybridisation probes, and in
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC probes used in the exemplification of the present invention.
XX
SQ Sequence 2454 BP; 835 A; 432 C; 417 G; 770 T; 0 other;
Query Match 100.0%; Score 2454; DB 24; Length 2454;
Best Local Similarity 100.0%; Pred No. 0;
Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGACTAATCTGTGGAGCAGTTTATTCAGTATPACCCAGGGTGCAGCCACACAGGACT 60
Db 1 GGACTAATCTGTGGAGCAGTTTATTCAGTATPACCCAGGGTGCAGCCACACAGGACT 60
QY 61 GTGTTCAAGGGTGTCTTTTCTTTTAAATGTAATACCTCTCTCATCTTTTCTTTACAC 120
Db 61 GTGTTCAAGGGTGTCTTTTCTTTTAAATGTAATACCTCTCTCATCTTTTCTTTACAC 120
QY 121 AGTGCTGAGACATTATACATTATAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 180
Db 121 AGTGCTGAGACATTATACATTATAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 180
QY 181 GGAGGACTACTCTCTCTGACAGTCTAGACAGTCTCTTACACTAAGACACCATGAAG 240
Db 181 GGAGGACTACTCTCTCTGACAGTCTAGACAGTCTCTTACACTAAGACACCATGAAG 240
QY 241 AGTATGTCTCTTATTTATTCCTGGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 241 AGTATGTCTCTTATTTATTCCTGGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 ACATCGCACTGAAGAATATGATGCTGAAGATATGAAGACACAGATGATGATGATGATG 360
Db 301 ACATCGCACTGAAGAATATGATGCTGAAGATATGAAGACACAGATGATGATGATGATG 360
QY 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Db 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 421 GCCATTTTTCATTTGATGCTGTTTCCAAATGTCCTTCTTTTCCAAACAGAGAGAGAG 480
Db 421 GCCATTTTTCATTTGATGCTGTTTCCAAATGTCCTTCTTTTCCAAACAGAGAGAGAG 480
QY 481 GAGTTCTACATGCTCAGATTTAGGTTTGACCTCAGTCCCAACCAACATTTCCATTTGATA 540
Db 481 GAGTTCTACATGCTCAGATTTAGGTTTGACCTCAGTCCCAACCAACATTTCCATTTGATA 540
QY 541 CTGCAATGCTTGATCTTCAAAACAATAAATAAAGAAATCAAGAAATGATTTTAAAG 600
Db 541 CTGCAATGCTTGATCTTCAAAACAATAAATAAAGAAATCAAGAAATGATTTTAAAG 600
QY 601 GACTCACTTCACTTTATGGTCTGATCCTGAACAAACAAAGCTTAACGAGATTCACCCAA 660
Db 601 GACTCACTTCACTTTATGGTCTGATCCTGAACAAACAAAGCTTAACGAGATTCACCCAA 660
QY 661 AAGCCTTTTCAACCAAGAAAGTTGCGAGAGGCTGTATCTGTCCCAACATCAACTAAGTG 720
Db 661 AAGCCTTTTCAACCAAGAAAGTTGCGAGAGGCTGTATCTGTCCCAACATCAACTAAGTG 720
QY 721 AATATCCACTTAATCTTCCCAATCATTTAGCAGAACTCAGAAATCATGATAAATAAAGTTA 780
Db 721 AATATCCACTTAATCTTCCCAATCATTTAGCAGAACTCAGAAATCATGATAAATAAAGTTA 780

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Db 721 AATACCCTTAATCTCCCAATCATTAGCAGAACTCAGAAATTCATGAAATAAAGTTA 780
Qy 781 AGAAATACAAAGACACATTCAAAGGAATGCTTTACACGCTTTGGAAATGAGTG 840
Db 781 AGAAATACAAAGACACATTCAAAGGAATGCTTTACACGCTTTGGAAATGAGTG 840
Qy 841 CAACCCCTTGATTAATATGAGATAGACCCAGGGCAATTTCAAGGGGTGACGGTGTCC 900
Db 841 CAACCCCTTGATTAATATGAGATAGACCCAGGGCAATTTCAAGGGGTGACGGTGTCC 900
Qy 901 ATATCAGAATTCGAGAAGCAAACTGACCTCAGTTCCTAAAGGCTTACCAACCACTTAT 960
Db 901 ATATCAGAATTCGAGAAGCAAACTGACCTCAGTTCCTAAAGGCTTACCAACCACTTAT 960
Qy 961 TGGAGCTTCACCTAGATATATAAATAATTCACAGTGGAACTTCAGGATTTTAAACGAT 1020
Db 961 TGGAGCTTCACCTAGATATATAAATAATTCACAGTGGAACTTCAGGATTTTAAACGAT 1020
Qy 1021 ACAAGAACTACAAAGGCTGGGCTTAGGAACAACAATAACACATATCGAAATGGGA 1080
Db 1021 ACAAGAACTACAAAGGCTGGGCTTAGGAACAACAATAACACATATCGAAATGGGA 1080
Qy 1081 GTCCTGCTAACATACCACTGTCGAGAGAAATACATTTGGAAAAACAATAAACAATAA 1140
Db 1081 GTCCTGCTAACATACCACTGTCGAGAGAAATACATTTGGAAAAACAATAAACAATAA 1140
Qy 1141 TCCCTTCAGGATTCACAGATGGAATACCTCCAGATATCTTCCTCATCTAATTCAA 1200
Db 1141 TCCCTTCAGGATTCACAGATGGAATACCTCCAGATATCTTCCTCATCTAATTCAA 1200
Qy 1201 TTGCAAGAGTGGAGTAATGACTTCGTCCCAACAGTCCCAAGATGAAGAATCTTTAT 1260
Db 1201 TTGCAAGAGTGGAGTAATGACTTCGTCCCAACAGTCCCAAGATGAAGAATCTTTAT 1260
Qy 1261 ACAGTSCAATAAGTTTATTCACAAACCCGGTGAATACTGGAAATGCAACCTGCAACAT 1320
Db 1261 ACAGTSCAATAAGTTTATTCACAAACCCGGTGAATACTGGAAATGCAACCTGCAACAT 1320
Qy 1321 TTCGTTGGTTTGGAGCAGATGAGTGTTCAGCTTGGGAACCTTGGAAATGAATATAG 1380
Db 1321 TTCGTTGGTTTGGAGCAGATGAGTGTTCAGCTTGGGAACCTTGGAAATGAATATAG 1380
Qy 1381 TAATTTGGTAATCTCCATTTAATATAAGATTCAAAATCCCTACATTTGGAATACCTGAAC 1440
Db 1381 TAATTTGGTAATCTCCATTTAATATAAGATTCAAAATCCCTACATTTGGAATACCTGAAC 1440
Qy 1441 TCTATTAATAATGGTAGTATTATATACAAACCAATATCTTCTCAAGTGGTAACTCC 1500
Db 1441 TCTATTAATAATGGTAGTATTATATACAAACCAATATCTTCTCAAGTGGTAACTCC 1500
Qy 1501 ACTGACTTATTTATGACAGAAATTTCAACGGAAATTTGCGAAACTATGATACATAG 1560
Db 1501 ACTGACTTATTTATGACAGAAATTTCAACGGAAATTTGCGAAACTATGATACATAG 1560
Qy 1561 GGGTTGAGAGAAACAAGATCTATTGCGAGTTCCTTTTGGCTACAAATGATCTTACATA 1620
Db 1561 GGGTTGAGAGAAACAAGATCTATTGCGAGTTCCTTTTGGCTACAAATGATCTTACATA 1620
Qy 1621 AATCTCATGCTTGACCATTCCTTTCTCATACAAAAAGTAAGATATTCGGTATTTAAC 1680
Db 1621 AATCTCATGCTTGACCATTCCTTTCTCATACAAAAAGTAAGATATTCGGTATTTAAC 1680
Qy 1681 ACTTTGTTATCAAGCACATTTTAAAGACATGCTAGTAAATGGAATGCTTGACTTAGC 1740
Db 1681 ACTTTGTTATCAAGCACATTTTAAAGACATGCTAGTAAATGGAATGCTTGACTTAGC 1740
Qy 1741 AAAATTTGCTCTTTCTATTTCTGCTGTAGAAAAACAAGATTAACAAGACAGTAATGGA 1800
Db 1741 AAAATTTGCTCTTTCTATTTCTGCTGTAGAAAAACAAGATTAACAAGACAGTAATGGA 1800
Qy 1801 AGAGTGCAATTACACTATCTTATTTCTTTAGTAACCTTGGGTAGTACTGTAATATTTTAA 1860
Db 1801 AGAGTGCAATTACACTATCTTATTTCTTTAGTAACCTTGGGTAGTACTGTAATATTTTAA 1860
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Qy 1861 CATCTTAAAGTATGATTTGATATAATCTTATTGAAATTTACCTTATCATGTCTTAGAGCCC 1920
Db 1861 CATCTTAAAGTATGATTTGATATAATCTTATTGAAATTTACCTTATCATGTCTTAGAGCCC 1920
Qy 1921 GTCCTTATGTTTAAAGCACTAATTTCTTAAATTTAAAGCCCTTCAGTAAATGCTTCAATACCAAC 1980
Db 1921 GTCCTTATGTTTAAAGCACTAATTTCTTAAATTTAAAGCCCTTCAGTAAATGCTTCAATACCAAC 1980
Qy 1981 TTGATAAATGCTACTCATAAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTA 2040
Db 1981 TTGATAAATGCTACTCATAAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTA 2040
Qy 2041 ATTATTACCTCATTTAAAAATCTCTGTAAACACGTGTAGTCTTTCATAAAATCTGTAAT 2100
Db 2041 ATTATTACCTCATTTAAAAATCTCTGTAAACACGTGTAGTCTTTCATAAAATCTGTAAT 2100
Qy 2101 CGCATTTTAAATGATCCCGCTATTATAAGCTTTTAAATAGCATGAAATTTAGGCTATATA 2160
Db 2101 CGCATTTTAAATGATCCCGCTATTATAAGCTTTTAAATAGCATGAAATTTAGGCTATATA 2160
Qy 2161 ACATTGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGTG 2220
Db 2161 ACATTGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGTG 2220
Qy 2221 GAAGAGCTGCACACTACAAATTTACACCAAAATTTCTCTTCAAAATACGTATGAGCTGG 2280
Db 2221 GAAGAGCTGCACACTACAAATTTACACCAAAATTTCTCTTCAAAATACGTATGAGCTGG 2280
Qy 2281 ATAACCTCTGAGAAACACATCTAGTATATACTGAATAAGCAGAGCATCAAAATTAACAGACA 2340
Db 2281 ATAACCTCTGAGAAACACATCTAGTATATACTGAATAAGCAGAGCATCAAAATTAACAGACA 2340
Qy 2341 GAAACCGAAAGCTCTATATAAAATGCTCAGAGTCTCTTATGATTTCTTTATGGCAATCAA 2400
Db 2341 GAAACCGAAAGCTCTATATAAAATGCTCAGAGTCTCTTATGATTTCTTTATGGCAATCAA 2400
Qy 2401 CATATGTAATAATCAGAAACAGGAAATTTTCATTAATAATATGGTTTGAAT 2454
Db 2401 CATATGTAATAATCAGAAACAGGAAATTTTCATTAATAATATGGTTTGAAT 2454
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RESULT 5

AAA49551
ID AAA49551 standard; cDNA; 2455 BP.

XX AAA49551;

XX 25-SEP-2000 (first entry)

XX Human PRO241 cDNA.

XX PRO; membrane bound protein; secreted protein; PRO357; PRO327;
KW PRO243; PRO715; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347;
KW PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide;
KW antibody; screening; detection; inhibition; probe; primer; human;
KW ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH CDS 234..1373

FT /*tag= a
FT /product= PRO241 polypeptide

XX WO200032776-A2.

XX 08-JUN-2000.

XX 01-DEC-1999; 99WO-US28301.

XX 01-DEC-1998; 98WO-US25108.

PR 16-DEC-1998; 98US-0112850.

Db 1681 CACTTTGTTATCAAGCACAATTTTAAAGAACTGTACTGTAAATGGAAATGCTTGTACTTAG 1740
Qy 1740 CAAATTTTGTCTCTTTCATTTGCTGTGAGAAAACAGAAATTAACAAGACAGTAATGTG 1799
Db 1741 CAAATTTTGTCTCTTTCATTTGCTGTGAGAAAACAGAAATTAACAAGACAGTAATGTG 1800
Qy 1800 AAGAGTGCATACACTATTCATTTCTTTTGTAGTAACTTTGGGTAGTACTGTAAATTTTAA 1859
Db 1801 AAGAGTGCATACACTATTCATTTCTTTTGTAGTAACTTTGGGTAGTACTGTAAATTTTAA 1860
Qy 1860 TCATCTTAAAGTATGATTTGATATAATCTTATTTGAAATTAACCTATCATGCTTTAGAGCC 1919
Db 1861 TCATCTTAAAGTATGATTTGATATAATCTTATTTGAAATTAACCTATCATGCTTTAGAGCC 1920
Qy 1920 CGTCTTTATGTTTAAACTATTTCTTTTAAATTAAGCTTTTCAAGTAAATGTTTCATTACCAA 1979
Db 1921 CGTCTTTATGTTTAAACTATTTCTTTTAAATTAAGCTTTTCAAGTAAATGTTTCATTACCAA 1980
Qy 1980 CTTGATAAATGCTACTACTAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTT 2039
Db 1981 CTTGATAAATGCTACTACTAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTT 2040
Qy 2040 AATATTACCTGATTTAAATCTCTGTAAAGCTGTAGTCTTCATAAAATCTGTAAAC 2099
Db 2041 AATATTACCTGATTTAAATCTCTGTAAAGCTGTAGTCTTCATAAAATCTGTAAAC 2100
Qy 2100 TCGCATTTTAAATGATCGCTTATTAAGCTTTTAAATGATGAAATGTTTGGCTATAT 2159
Db 2101 TCGCATTTTAAATGATCGCTTATTAAGCTTTTAAATGATGAAATGTTTGGCTATAT 2160
Qy 2160 AACATGCGCACTCAACTCTAAGAAATPATTTTTGGAGATATCCCTTTTGAAGACCTTGCCT 2219
Db 2161 AACATGCGCACTCAACTCTAAGAAATPATTTTTGGAGATATCCCTTTTGAAGACCTTGCCT 2220
Qy 2220 GGAAGAGCTGGACACTAACAATCTACACCAATTTGCTCTTCAATATGCTATGGACTG 2279
Db 2221 GGAAGAGCTGGACACTAACAATCTACACCAATTTGCTCTTCAATATGCTATGGACTG 2280
Qy 2280 GATAACTCTGAGAAACACATCTAGTATACTGAATAAGCAGAGCATCAAAATTAACACAGAC 2339
Db 2281 GATAACTCTGAGAAACACATCTAGTATACTGAATAAGCAGAGCATCAAAATTAACACAGAC 2340
Qy 2340 AGAAACCGAAGCTCTATATAAATGCTCAGAGTCTTTTATGATTTCTTATTTGGCAATCA 2399
Db 2341 AGAAACCGAAGCTCTATATAAATGCTCAGAGTCTTTTATGATTTCTTATTTGGCAATCA 2400
Qy 2400 ACATATCTAAATCAGAAACAGGAAATTTTCATTAAATAATTTGGTTTCAAT 2454
Db 2401 ACATATCTAAATCAGAAACAGGAAATTTTCATTAAATAATTTGGTTTCAAT 2455

JLT 6

18405
ID AAH18405 standard; cdNA; 2089 BP.
XX
AC AAH18405;
XX
DF 26-JUN-2001 (first entry)
XX
DE Human cdNA sequence SEQ ID NO:18472.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
FN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX (HELI-) HELIX RES INST.
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs
XX
PS Claim 8; SEQ ID 18472; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 2089 BP; 712 A; 356 C; 352 G; 669 T; 0 other;

Query Match 72.8%; Score 1786.8; DB 22; Length 2089;
Best Local Similarity 89.3%; Pred. No. 0;
Matches 2075; Conservative 0; Mismatches 2; Indels 247; Gaps 4;

Qy 143 ATAGATAAGTAGTAGTACATGGTGGATACCTTCTTACCTTTTAGGAGGACTACTCTCTTCTGACA 202
Db 1 ATAGATAAGTAGTAGTACATGGTGGATACCTTCTTACCTTTTAGGAGGACTACTCTCTTCTGACA 60
Qy 203 GTCCTAGACTGGTCTTCTACACTAAGACACCATGAGGAGTATGCTCTCTTATTTCTCT 262
Db 61 GTCCTAGACTGGTCTTCTACACTAAGACACCATGAGGAGTATGCTCTCTTATTTCTCT 120
Qy 263 GGCCTTTGTGCTCTGCCAAACCTTCTTTAGCCCTTCACATCCACTCCAGGAATATGAT 322
Db 121 GGCCTTTGTGCTCTGCCAAACCTTCTTTAGCCCTTCACATCCACTCCAGGAATATGAT 180
Qy 323 GCTGAAGGATATGGAAGACACA-----GATGATGATGATGATGATGATGATGATGATGA 370
Db 181 GCTGAAGGATATGGAAGACACA-----GATGATGATGATGATGATGATGATGATGATGA 240
Qy 371 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGA 430
Db 241 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGA 300
Qy 431 TCCATTTGATCTGTTTCCATGTCCTCATTTGGAGTGCAGTGCATTTCCAGAGTTGTGACA 490
Db 301 TCCATTTGATCTGTTTCCATGTCCTCATTTGGAGTGCAGTGCATTTCCAGAGTTGTGACA 360
Qy 491 TTGCTCAGATTTAGGTTTGGACCTCAGTCCCAACACATTCATTTTGTGATCTACTCGAATGCT 550
Db 491 TTGCTCAGATTTAGGTTTGGACCTCAGTCCCAACACATTCATTTTGTGATCTACTCGAATGCT 550

361	TTGCTCAGATTTAGGTTTGACCTGACTGCCAACCAACATTCCTCATTTGATCTACTCGGAATGCT	420
551	TGATCTTCAAAACAATAAATTAAGGAAATCAAGAAATGATTTTAAAGGACTCACTTC	610
421	TGATCTTCAAAACAATAAATTAAGGAAATCAAGAAATGATTTTAAAGGACTCACTTC	480
611	ACTTTATGGTCTGATCCTGAACAACAACAGCTTAACGAAGATTCACCCAAAAGCCTTTCT	670
481	ACTTTATGGTCTGATCCTGAACAACAACAGCTTAACGAAGATTCACCCAAAAGCCTTTCT	540
671	AACCCAAAGAACTGCGAAGGCTGTATCTGTGCCACAATCAACTAAGTGAATATCCACT	730
541	AACCCAAAGAACTGCGAAGGCTGTATCTGTGCCACAATCAACTAAGTGAATATCCACT	600
731	TAATCTTCCAAATCAATTAGCAGAACTCAGAAATTCATGAAAATAAAGTTAAAGAAAATACA	790
601	TAATCTTCCAAATCAATTAGCAGAACTCAGAAATTCATGAAAATAAAGTTAAAGAAAATACA	660
791	AAGGACACATTCAAAGGAATGAATGCTTTACAGTTTGGAAATGAGTGCAACCCCTCT	850
661	AAAGGACACATTCAAAGGAATGAATGCTTTACACGTTTGGAAATGAGTGCAACCCCTCT	720
851	TGATAATAATGGGATAGAGCGAGGCGCATTTGAAGGGTGACGGTGTCCCATATCAGAAT	910
721	TGATAATAATGGGATAGAGCGAGGCGCATTTGAAGGGTGACGGTGTCCCATATCAGAAT	780
911	TGCAGAGCAAAACTGACCTCAGTTCTCTAAAGGCTTACCACCAACTTTATTGGAGCTTCA	970
781	TGCAGAGCAAAACTGACCTCAGTTCTCTAAAGGCTTACCACCAACTTTATTGGAGCTTCA	810
971	CTTAGATTAATAAATAATTTCAACAGTGGAACTTGAGGATTTTAAACGATACAAAGAACT	1030
811	-----	810
1031	ACAAAGCCTGGCCTAGGAACAACAATAACAGATATCGAAAATGGGAGTCTTCTCTAA	1090
811	-----	810
1091	CATACCACGTTGAGAGAAATACATTTGGAAAACAATAAACTAAAAAAATCCCTTCAGG	1150
811	-----	810
1151	ATTACCAGATTGAATACCTCCAGATAATCTTTCCTTCATTCTAATTCAAATTCGAAGAT	1210
811	-----AGATAAATCTTCCCTTCATTCTAATTCAAATTCGAAGAT	847
1211	GGGAGTAAATGACTTCTGTCCAAAGTGCACAAAGATGAAGAAATCTTTATACAGTGAAT	1270
848	GGGAGTAAATGACTTCTGTCCAAAGTGCACAAAGATGAAGAAATCTTTATACAGTGAAT	907
1271	AAGTTTATTCACAAACCCGGTGAATACTGGGAAATGCAACCTTGCACATTTTCGTTGTGT	1330
908	AAGTTTATTCACAAACCCGGTGAATACTGGGAAATGCAACCTTGCACATTTTCGTTGTGT	967
1331	TTTGAGCAGAAATGAGTGTTTCAGCTTGGGAATCTTTGGAAATGAATAATATAGTAATTCGTA	1390
968	TTTGAGCAGAAATGAGTGTTTCAGCTTGGGAATCTTTGGAAATGAATAATATAGTAATTCGTA	1027
1391	TGTCCTATTAATATAAGATTCAAAATCCCTACATTTGGAAATCTTGAACCTCTTAAATA	1450
1028	TGTCCTATTAATATAAGATTCAAAATCCCTACATTTGGAAATCTTGAACCTCTTAAATA	1087
1451	ATGGTAGTATTATATACAAAGCAATATCTATTTCTCAAGTGGTGAAGTCCACGTACTTAT	1510
1088	ATGGTAGTATTATATACAAAGCAATATCTATTTCTCAAGTGGTGAAGTCCACGTACTTAT	1147
1511	TTTATCACAAAGAAATTTCAACGGAAATTTTGCCAAACTATTGATACATAAAGGGGTTGAGAG	1570
1148	TTTATCACAAAGAAATTTCAACGGAAATTTTGCCAAACTATTGATACATAAAGGGGTTGAGAG	1206
1571	AAACAACATCTATTCAGTTTCCTTTTTCGGTACAAATGATCTTACATAAATCTCATGC	1630
1207	AAACAACATCTATTCAGTTTCCTTTTTCGGTACAAATGATCTTACATAAATCTCATGC	1265

1631	Qy	TTGACCAATTCCTTTCTTCATACACAAAAAGTAAGATATTCGGTATTTAAACACATTTGGTTAT	1690
1266	Db	TTGACCAATTCCTTTCTTCATACACAAAAAGTAAGATATTCGGTATTTAAACACATTTGGTTAT	1325
1691	Qy	CAAGCACATTTTAAAAAGAACTGACTGTAATAATGGAATGCTTGACTTTAGCAAAATTTGTG	1750
1326	Db	CAAGCATATTTTAAAAAGAACTGACTGTAATAATGGAATGCTTGACTTTAGCAAAATTTGTG	1385
1751	Qy	CTCTTTTCATTTGCTTTAGAAAAACAGAAATTAACAAAGACAGTAANTGTGAAGAGTGCATT	1810
1386	Db	CTCTTTTCATTTGCTTTAGAAAAACAGAAATTAACAAAGACAGTAANTGTGAAGAGTGCATT	1445
1811	Qy	ACACTATTCATTATTCCTTTAGTAACCTGGGTAGTACTGCTAATATTTTAAATCATCTTAAAG	1870
1446	Db	ACACTATTCATTATTCCTTTAGTAACCTGGGTAGTACTGCTAATATTTTAAATCATCTTAAAG	1505
1871	Qy	TATGATTTGATAAATCTTATGAAATTAACCTTATCATGCTTAGAGCCCGTCTTTATGT	1930
1506	Db	TATGATTTGATAAATCTTATGAAATTAACCTTATCATGCTTAGAGCCCGTCTTTATGT	1565
1931	Qy	TTAAAACTAATTTCTTTAAAAATAAAGCCCTTCAGTAAATGTTTCATTACCACTTGATAAATG	1990
1566	Db	TTAAAACTAATTTCTTTAAAAATAAAGCCCTTCAGTAAATGTTTCATTACCACTTGATAAATG	1625
1991	Qy	CTACTCATAGAGCTGCTTTGGGGCTATAGCATATGCTTTTATTTTAAATATTATACCT	2050
1626	Db	CTACTCATAGAGCTGCTTTGGGGCTATAGCATATGCTTTTATTTTAAATATTATACCT	1685
2051	Qy	GATTTAAAAATCTCTGTAAAAACGCTGTAGTGTTTTCATAAAACTGTAACTCGCATTTTAA	2110
1686	Db	GATTTAAAAATCTCTGTAAAAACGCTGTAGTGTTTTCATAAAACTGTAACTCGCATTTTAA	1745
2111	Qy	TGATCCGCTATATTAAGCTTTTAAAGCATGAAATTTGTAGGCTATATTAACATTGGCCAC	2170
1746	Db	TGATCAGCTATATTAAGCTTTTAAAGCATGAAATTTGTAGGCTATATTAACATTGGCCAC	1805
2171	Qy	TTCAACTCTAAGGAATATTTTGGAGATATCCCTTTTGGAAAGACCTTGCTTGAAGAGCGTG	2230
1806	Db	TTCAACTCTAAGGAATATTTTGGAGATATCCCTTTTGGAAAGACCTTGCTTGAAGAGCGTG	1865
2231	Qy	GACACTAACAAATTCACACCAAAATGTCTCTTCAAAATACGCTATGGACTGGATACTCTGA	2290
1866	Db	GACACTAACAAATTCACACCAAAATGTCTCTTCAAAATACGCTATGGACTGGATACTCTGA	1925
2291	Qy	GAACACATCTAGTATAACTGCAATAACGACAGAGCATCAAAATTAACACAGACAGAAACCGAAA	2350
1926	Db	GAACACATCTAGTATAACTGCAATAACGACAGAGCATCAAAATTAACACAGACAGAAACCGAAA	1985
2351	Qy	GCTCTATATAAATGCTCAGAGTCTCTTTATGTATTTCTTATTTGGCATTTCAACATATGTAAA	2410
1986	Db	GCTCTATATAAATGCTCAGAGTCTCTTTATGTATTTCTTATTTGGCATTTCAACATATGTAAA	2045
2411	Qy	ATCAGAAAAACGGGAAATTTTCATTTAAAAATATTGGTTTGAAT	2454
2046	Db	ATCAGAAAAACGGGAAATTTTCATTTAAAAATATTGGTTTGAAT	2089

RESULTS

AA533113

ID AAS33113 standard; cDNA: 1674 BP

XX

AC AAS33113;

XX

DT 04-DEC-2001 (first entry)

XX

DE DNA encoding human secreted protein, Seq ID No 72.

XX

KW Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina
KW Rheumatoid arthritis; antiarteriosclerotic; cardiac; vascular;
KW cerebroprotective; thrombolytic; antimicrobial; ophthalmological;
KW cystostatic; Alzheimer's disease; Parkinson's disease; human; cancer;
KW multiple sclerosis; cancer; hyperproliferative disorder; infection;
KW

KW Gaucher's disease; neurological disease; cerebrovascular disorder;
KW thrombosis; wound healing; ss.

OS Homo sapiens.

XX
PN
W0200155326-A

XX

XX

7-7 XXX
T T
NEUO T
T O C
C M T
C C C
C C C

PR 31-JAN-2000; 2000US-01/9063.
XX

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;

DR WPI; 2001-451931/48.

XX
DR P-PSDB; AAU20404.

PT New nucleic acids

...

CLAIM 1, SEQ ID NO 12, 13PP, ENGLISH

the invention relates to novel isolated nucleic acid molecules (I) encoding human secreted proteins (II). (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate expression of secreted proteins. (I) and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and so which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of the secreted proteins. The anti-(II) antibodies and antagonists may also be used to down regulate expression and activity of (II). The anti-(II) antibodies may also be used as diagnostic agents for detecting the presence of (II) in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease and Charcot-Marie-Tooth disease), cardio-/cerebrovascular disorders (e.g. cardiac arrest, tachycardia, angina and thrombosis), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). (I) and (II), agonists, antagonists and antibodies can also be used to promote wound healing, maintain organs before transplantation, and support cell culture of primary tissues. AAS33043-AAS33486 represent human secreted protein coding sequences, PCR primers, and related sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification but was obtained in electronic format directly from WIPO at: [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

Sequence 1674 BP; 602 A; 266 C; 274 G; 528 T; 4 other; XX

Query Match 62.1%; Score 1524; DB 22; Length 1674;
Best Local Similarity 98.3%; Pred. No. 1.4e-309;
Matches 1574; Conservative 4; Mismatches 19; Indels 4;

854 TAATAATGGGATAGAGCCAGGGGCATTGAAGGGGTGACGGTGTTCATATCAGAAATTGC 913 QY

Db
66 TGATAATAATGGATAGAGCCAGGGCATTGAAGGGTGACGGTG-TCCATATCAGAATTGC 124

914 AGAAGCAAAACTGACCTCAGTTCCTAAAGGCTTACCACCAACTTTATTGGAGGCTTCACCT 973

[illegible][illegible]

185	Db		AGATTATAAATAA-TTCAACAGTGGAACTTGGAGAYTTTAAACGATWCAAGAACA	243
1034	Qy		AAGSCTGGGCTTAGGAACAACAAAATCAGAGATATCGAAAATGGGAGTCTTGCTAACAT	1093
244	Db		AAGSCTGGGCTTAGGAACAACAAAATCAGAGATATCGAAAATGGGAGTCTTGCTAACAT	303
1094	Qy		ACCAGTGTGAGAGAAATACATTTGGGAAACAAATAAACAATAAATAAATAAATCCCTTCAGATT	1153
304	Db		ACCAGTGTGAGAGAAATACATTTGGGAAACAAATAAACAATAAATAAATAAATCCCTTCAGATT	363
1154	Qy		ACCAGAGTGAATAACCTCCAGATAATCTTCCTTCATTTCAATTCATTCGAACAGTGGG	1213
364	Db		ACCAGAGTGAATAACCTCCAGATAATCTTCCTTCATTTCAATTCGAACAGTGGG	423
1214	Qy		AGTAAATGACTTCTGTCCACAGTGCACAAAGATGAAGAAATCTTTATACAGTGAATAAG	1273
424	Db		AGTAAATGACTTCTGTCCACAGTGCACAAAGATGAAGAAATCTTTATACAGTGAATAAG	483
1274	Qy		TTTATTCACAACACCCGGTGAAATACTGGGAAATCGAAGTGCACATTTCCGTGTGTTTT	1333
484	Db		TTTATTCACAACACCCGGTGAAATACTGGGAAATCGAAGTGCACATTTCCGTGTGTTTT	543
1334	Qy		GAGCAGAAATGAGTCTCAGCTTGGGAACTTTGGAAATCTGAACCTCTATTAATGTAATGT	1393
544	Db		GAGCAGAAATGAGTCTCAGCTTGGGAACTTTGGAAATCTGAACCTCTATTAATGTAATGT	603
1394	Qy		CCATTTAATATAAGATTCAAAATCCCTACATTTTGGAAATCTGAACCTCTATTAATGTAATGT	1453
604	Db		CCATTTAATATAAGATTCAAAATCCCTACATTTTGGAAATCTGAACCTCTATTAATGTAATGT	663
1454	Qy		GTAGTATTATATACAAAGCAAAATATCTATTTCTCAAGTGGTGAAGTCCACTGACATTTTT	1513
664	Db		GTAGTATTATATACAAAGCAAAATATCTATTTCTCAAGTGGTGAAGTCCACTGACATTTTT	723
1514	Qy		ATGCACAGAAATTTCAACGGAAATTTTGCCAAACATTTGATACATTAAGGGTTGAGAGAA	1573
724	Db		ATGCACAGAAATTTCAACGGAAATTTTGCCAAACATTTGATACATTAAGGGTTGAGAGAA	782
1574	Qy		CAAGCATCTATTGTCAGTTTCCCTTTTGGCGTCAAAATGATCTTACATAATCTCATGCTTG	1633
783	Db		CAAGCATCTATTGTCAGTTTCCCTTTTGGCGTCAAAATGATCTTACATAATCTCATGCTTG	841
1634	Qy		ACCATTCCTTTCTTCATAACAAAAAGTAAGATATTCGGTATTTAAACACTTTGTTATCAA	1693
842	Db		ACCATTCCTTTCTTCATAACAAAAAGTAAGATATTCGGTATTTAAACACTTTGTTATCAA	901
1694	Qy		GCACATTTTAAAGAAGACTGTACTGTAAATGGAAATGCTTGTAGCAAAAATTTGTGCTC	1753
902	Db		GCATATTTTAAAGAAGACTGTACTGTAAATGGAAATGCTTGTAGCAAAAATTTGTGCTC	961
1754	Qy		TTTTCATTTGCTGTAGAAAAACAGAAATTAACAAAGACAGTAATCTGAAGAGTGCATTAACA	1813
962	Db		TTTTCATTTGCTGTAGAAAAACAGAAATTAACAAAGACAGTAATCTGAAGAGTGCATTAACA	1021
1814	Qy		CTATTCCTTATCTTTAGTAACTTGGGTAGTACTGTAAATTTTTTAATCATCTTAAAGTAT	1873
1022	Db		CTATTCCTTATCTTTAGTAACTTGGGTAGTACTGTAAATTTTTTAATCATCTTAAAGTAT	1081
1874	Qy		GATTTGATATAATCTTATTGAAATTAACCTTATCATGCTTTAGAGCCGCTCTTTATGTTTA	1933
1082	Db		GATTTGATATAATCTTATTGAAATTAACCTTATCATGCTTTAGAGCCGCTCTTTATGTTTA	1141
1934	Qy		AAACTAATTTCTTAAAATAAGCCCTCAGTAATGTTTCATTTACCACCTTGATAATGCTA	1993
1142	Db		AAACTAATTTCTTAAAATAAGCCCTCAGTAATGTTTCATTTACCACCTTGATAATGCTA	1201
1994	Qy		CTCATAAGAGCTGTTTGGGGCTATAGCATATGCTTTTTTTTTTTTAAATTTACCTGAT	2053
1202	Db		CTCATAAGAGCTGTTTGGGGCTATAGCATATGCTTTTTTTTTTTTAAATTTACCTGAT	1261
2054	Qy		TTAAAAATCTCTGTAAAAACGCTAGTGTTCATAAAAATCTGTAACTCGCATTTTAAATGA	2113

714	Qy	CTAAGTGAATATCACACTTAATCTTCCAAATCAATTAGCAGAACTCAGAAATTCATGAAAT	773
785	Db	CTAAGTGAATATCACACTTAATCTTCCAAATCAATTAGCAGAACTCAGAAATTCATGAAAT	844
774	Qy	AAAGTTAAGAAAATACAAAAGGACACATTCAAAGGAATGAATGCTTTACACGTTTTCGAA	833
845	Db	AAAGTTAAGAAAATACAAAAGGACACATTCAAAGGAATGAATGCTTTACACGTTTTCGAA	904
834	Qy	ATGAGTGCAAACCTCTTGATATAATATGGATAGAGCCAGGGGCATTTGAAGGGGTGACG	893
905	Db	ATGAGTGCAAACCTCTTGATATAATATGGATAGAGCCAGGGGCATTTGAAGGGGTGACG	964
894	Qy	GTGTTCCATATCAGAAATTCGAGAAGCAAAACTGACCTCAGTTCTCTAAAGGCTTACCACCA	953
965	Db	GTGTTCCATATCAGAAATTCGAGAAGCAAAACTGACCTCAGTTCTCTAAAGGCTTACCACCA	1024
954	Qy	ACTTTATTGGAGCTTCACCTTAGATTATAATATAATTTCAACAGTGGAACTTTGAGGATTTT	1013
1025	Db	ACTTTATTGGAGCTTCACCTTAGATTATAATATAATTTCAACAGTGGAACTTTGAGGATTTT	1084
1014	Qy	AAACGATACAAAAGAACTTACAAAAGCTGGGCTTAGGAAAACAAAATCACAGATATCGAA	1073
1085	Db	AAACGATACAAAAGAACTTACAAAAGCTGGGCTTAGGAAAACAAAATCACAGATATCGAA	1144
1074	Qy	AATGGGAGCTTGCTTAACATACACACGCTGTGAGAGAAATACATTTGGAAAACAAATAACTA	1133
1145	Db	AATGGGAGCTTGCTTAACATACACACGCTGTGAGAGAAATACATTTGGAAAACAAATAACTA	1204
1134	Qy	AAAAAATCCCTTCAGGATTAACAGAGTTTCAAAATACCTCCAGATAATCTTCCCTTCATTCT	1193
1205	Db	AAAAAATCCCTTCAGGATTAACAGAGTTTCAAAATACCTCCAGATAATCTTCCCTTCATTCT	1264
1194	Qy	AATTCAAATTCGAAGAGTGGGAGTAAATGACTTCTGTCCAAACAGTGCCAAAAGATGAAGAAA	1253
1265	Db	AATTCAAATTCGAAGAGTGGGAGTAAATGACTTCTGTCCAAACAGTGCCAAAAGATGAAGAAA	1324
1254	Qy	TCCTTTATACAGTGCATAAGCTTTATTCAACAACCCGGTGAAATACTCGGGAATGCAACCT	1313
1325	Db	TCCTTTATACAGTGCATAAGCTTTATTCAACAACCCGGTGAAATACTCGGGAATGCAACCT	1384
1314	Qy	GCACATTTTCGTTGTTTTGACGAGAAATGAGTGTTCAGCTTGGGAACCTTTGGAAATGTAA	1373
1385	Db	GCACATTTTCGTTGTTTTGACGAGAAATGAGTGTTCAGCTTGGGAACCTTTGGAAATGTAA	1444
1374	Qy	TAATTAGTAATTGGTAATGTCCATTTAATATAGATTCAAAAATCCCTACATTTTGGGAATA	1433
1445	Db	TAATTAGTAATTGGTAATGTCCATTTAATATAGATTCAAAAATCCCTACATTTTGGGAATA	1504
1434	Qy	CTTGAACCTCTTAATTAATGGTATGATTAATATATACAAAGCAA	1476
1505	Db	CTTGAACCTCTTAATTAATGGGAGTATTAATATATACCAAGCAA	1547

DEC 11 1964

RESULT 9
AAS86756

AA586/56
ID AA586756 standard: cDNA: 1492 BP.

XX
ID
AAAS

AA
AC
AAS

XX
XX
XX

DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #22560.

XX XX

Human; chromosome mapping; gene mapping; gene therapy; forensic; KW

KW food

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX 9

PF 30-MAR-2001; 2001WO-US08631.

31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
(HYSE-) HYSEQ INC.
Drmanac RT, Liu C, Tang YT;
WPI; 2001-639362/73.
P-PSDB; ABG22569.
New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
biodiversity
Claim 1; SEQ ID No 22560; 103pp; English.
The invention relates to isolated polynucleotide (I) and
polypeptide (II) sequences. (I) is useful as hybridisation probes,
polymerase chain reaction (PCR) primers, oligomers, and for chromosome
and gene mapping, and in recombinant production of (II). The
polynucleotides are also used in diagnostics as expressed sequence tags
for identifying expressed genes. (I) is useful in gene therapy techniques
to restore normal activity of (II) or to treat disease states involving
(II). (II) is useful for generating antibodies against it, detecting or
quantitating a polypeptide in tissue, as molecular weight markers and as
a food supplement. (I) and its binding partners are useful in medical
imaging of sites expressing (II). (I) and (II) are useful for treating
disorders involving aberrant protein expression or biological activity.
The polypeptide and polynucleotide sequences have applications in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits to assess biodiversity
and to produce other types of data and products dependent on DNA and
amino acid sequences. AAS64197-AAS94564 represent novel human
diagnostic coding sequences of the invention.
Note: The sequence data for this patent did not appear in the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.

Sequence 1492 BP: 499 A: 279 C: 279 G: 435 T: 0 other;

QY 710 TCACTAGTGAATACACCTTAATCTTCCCAAAATCATTAGCAGAACTCAGAAATTCATGA 769
Db 696 CCAACTAGTGAATTCACCTTAATCTTCCCAAAATCATTAGCAGAACTCAGAAATTCATGA 755
QY 770 AAATAAGTTAAGAAATTAAGAAAGCAGACATTTCAAGGAATGAATGCTTTTACAGCTTTT 829
Db 756 TAATAAGTTAAGAAATTAAGAAAGCAGACATTTCAAGGAATGAATGCTTTTACATGTTTT 815
QY 830 GGAATAGTGCACCAACCTCTTGTATAAATTAAGGATAGAGCCAGGGGATTTGAAGGGGT 889
Db 816 GGAATAGTGCACCAACCTCTTGTAGAACACACGGGATAGAACCGGGGATTTGAAGGGGT 875
QY 890 GACGGTTTCCATATCAGAAATTCAGAAAGCAAACTGACCTCAGTTCCTTAAAGGCTTACC 949
Db 876 GACATTTTCCATATCAGAAATTCAGAAAGCAAACTGACCTCAGTTCCTTAAAGGCTTACC 935
QY 950 ACCAATTTATGGAGCTTCACTTAGATTATATAAATAATTCACAGTGGAACTTGAAGA 1009
Db 936 ACCAATTTTGTGGAGCTTCACTTAGATTATATAAATAATTCACAGTGGAACTTGAAGA 995
QY 1010 TTTTAAAGATACAAAGAACTACAAAGGCTGGGCTTAGGAAACAAACAAATCACAGATAT 1069
Db 996 TCTTAAAGATACAAAGAACTACAAAGGCTGGGCTTAGGAAACAAACAAATCACAGATAT 1055
QY 1070 CGAAATGGAGCTTGTGTAACATACACAGTGTGAGAAATACATTTGGAAACAAATAA 1129
Db 1056 TGAATGGAACTTTGTGTAATATACACAGTGTGAGAGATACACCTTGGAAACAAATAA 1115
QY 1130 ACTAAATAATCCCTTACAGGATACAGAGTTGAATACCTCCAGATATCTTCTTCA 1189
Db 1116 ACTAAATAATCCCTTACAGGATACAGAGTTGAATACCTCCAGATATCTTCTTCA 1175
QY 1190 TTCTAATCAATTCGAAGTGGGAGTAAATGACCTTCTGCAACAGTGCACCAAGATGAA 1249
Db 1176 TTATTAATCAATTCGAAGTGGGAGTAAATGACCTTCTGCAACAGTGCACCAAGATGAA 1235
QY 1250 GAAATCTTTATACAGTGCATTAAGTTATTCACAAACCCGGTGAATACCTGGAAATGCA 1309
Db 1236 GAAATCTTTATACAGTGCATTAAGTTATTCACAAACCCGGTGAATACCTGGAAATGCA 1295
QY 1310 ACCTGCAACATTTCTGTTTTCAGCAGATGAGTGTTCAGCTTGGGAATTTGGAT 1369
Db 1296 ACCTGCAACATTTCTGTTTTCAGCAGATGAGTGTTCAGCTTGGGAATTTGGAT 1354
QY 1370 GTAATAATTAAGTAAATGTTGATGCTTAAATTAAGATCAAAATCCCTACATTTGG 1429
Db 1355 -----ATAATTCATGACATCCATTAATATATAAATTCACAAATGTACATTTGG 1405
QY 1430 AATCTGAACTCTATTAAATGCTAGTATATATATACAGCAAAATATCTTCTCAA 1489
Db 1406 AATCTGAACTCTCTAGTAAATGCTAGTATATATACACATAAGCAAAATCTTCTCT 1462
QY 1490 GTGGTAACTGCACTGCTTATTTATGACAGAAATTTCAAGGAAATTTGGCAAACTAT 1549
Db 1463 -----ATATGTCATGACAAATAATTTCAACAGAAATTTGGCTAATAT 1507
QY 1550 TGATACATAAGGGTTGAGAGAAACAGCATCTATTGCTGCTTCTTTCGCTACAAT 1609
Db 1508 TGATGCTCA -----GAATAAATTTCTATTGCTGCTGCTTCTGCTGCTGCTGCTGCT 1555
QY 1610 GATCTTACATAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1669
Db 1556 ATCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1610
QY 1670 CGGTATTTAAGCACTTTGTTTCAAGCAGATTTTAAAGAAAGTCTGCTGCTGCTGCTGCTGCT 1729
Db 1611 TAGTATTTAAGCCTTCAATTAAG - TCAGTCAACAGAAATTTGCTGCTGCTGCTGCTGCTGCT 1668
QY 1730 CTGACTTTAGCAAAATTTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1789
Db 1669 CTGACTTTAGCAAAATTTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1727
QY 1790 CAGTAATGTAAGAGTGCATTAACATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1846

RESULT 13

AAI94377

ID AAI94377 standard; cDNA; 896 BP.

XX AAI94377;

DT 13-NOV-2001 (first entry)

XX Human neuroblastoma expressed polynucleotide SEQ ID NO 452.

XX Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.

XX Homo sapiens.

XX WO200166719-A1.

XX 13-SEP-2001.

XX 02-MAR-2001; 2001WO-JP01629.

XX 07-MAR-2000; 2000JP-0159195.

XX (CHIB-) CHIBA PREFECTURE.

XX (HISM) HISAMITSU PHARM CO LTD.

XX Nakagawara A;

XX WPI; 2001-565584/63.

XX Nucleic acids originating in gene expressed in human neuroblastoma,
PT useful as probe or primer in diagnosing prognosis of human
PT neuroblastoma, malignancy and susceptibility indicator or tumour marker
PT for anti-cancer agents

xx PS Claim 1; Page 377; 2979pp; Japanese.

xx CC The invention relates to novel genes (AAI93926-AAI97963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy and susceptibility indicators or tumour markers for anti-cancer agents. The CC CC gene information for diagnosing prognosis is related to factors similar to that for N-myc and TrkA genes.

xx SQ Sequence 896 BP; 340 A; 169 C; 162 G; 216 T; 9 other;

Query Match 32.28; Score 790.2; DB 22; Length 896;
Best Local Similarity 96.88; Pred. No. 5.3e-156;
Matches 834; Conservative 0; Mismatches 25; Indels 3; Gaps 3;

Qy 542 TCGAATGCTGATCTTCAAAACAATAAAATTAAGGAAATCAAGAAATGATTTAAAGG 601
Db 17 TGGCTTACTGATCTTCAAAACAATAAAATTAAGGAAATCAAGAAATGATTTAAAGG 76

Qy 602 ACTCAGTCTTATGCTGATCTTGAACAACAAGCTACGAGATTCACCCAAA 661
Db 77 ACTCAGTCTTATGCTGATCTTGAACAACAAGCTACGAGATTCACCCAAA 136

Qy 662 AGCCTTTTAAACCAAGAAGTTCGGAAGGCTGTATCTGTCCACAAATCAACTAAGTGA 721
Db 137 AGCCTTTTAAACCAAGAAGTTCGGAAGGCTGTATCTGTCCACAAATCAACTAAGTGA 196

Qy 722 AATACCACTTAATCTTCCAAATCATTTAGCAGAACTCAGAAATCATGAAATAAAGTTAA 781
Db 197 AATACCACTTAATCTTCCAAATCATTTAGCAGAACTCAGAAATCATGAAATAAAGTTAA 256

Qy 782 GAAATFACAAAGACACATTCAAAGAAATGAATGCTTTTACACGTTTGGAAATGAGTGC 841
Db 257 GAAATFACAAAGACACATTCAAAGAAATGAATGCTTTTACACGTTTGGAAATGAGTGC 316

Qy 842 AAACCCCTTGTGATAATGATGATAGAGGAGGAGGCTTTGAAGGGGTGAGGTTGCCA 901
Db 317 AAACCCCTTGTGATAATGATGATAGAGGAGGAGGCTTTGAAGGGGTGAGGTTGCCA 376

Qy 902 TATCAGAAATGCAGAAACAACTGACCTCAGTTCTTAAAGGCTTACCACCACTTTATT 961
Db 377 TATCAGAAATGCAGAAACAACTGACCTCAGTTCTTAAAGGCTTACCACCACTTTATT 436

Qy 962 GGAGCTTCACTTAGATTATATAAAATTTCAACAGTGGAACTTGAGGATTTTAAACGATA 1021
Db 437 GGAGCTTCACTTAGATTATATAAAATTTCAACAGTGGAACTTGAGGATTTTAAACGATA 496

Qy 1022 CAAGAAGTCAAGGCTGGGCTTAGGAACAACAAGAAATCAGAGATTCGAAATGGAG 1081
Db 497 CAAGAAGTCAAGGCTGGGCTTAGGAACAACAAGAAATCAGAGATTCGAAATGGAG 556

Qy 1082 TCTGTCTAACATACACCTGTGAG - AGAAATACATTTTGGAAACAAATAAATAAATAA 1140
Db 557 TCTGTCTAACATACACCTGTGAGAGAAATACATTTTGGGAACAATAAATAAATAA 616

Qy 1141 TCCCTTCAGGATFACC - AGAGTTGAAATACCTCC - AGATAATCTTCCTTCATCTAATC 1198
Db 617 TCCCTTCAGGATFACCAGAGTTGAAATACCTTCAAGATAATCTTCCTTCATCTAATC 676

Qy 1199 AATGCAAGAGTGGAGTAAATGACTTCTGTCCACAGTCCCAAGATGAAGAAATCTTT 1258
Db 677 AATGCAAGAGTGGAGTAAATGACTTCTGTCCACAGTCCCAAGATGAAGAAATCTTT 736

Qy 1259 ATACAGTGCATTAAGTTTATTTCAACACCCGGTGAATATCTGGGAAATGCAACCTGCAAC 1318
Db 737 ATACAGTGCATTAAGTTTATTTCAACACCCNGTGAATATCTGGGAAATGCAACCTGCAAC 796

Qy 1319 ATTTGCTGTGTTTGTAGCAGAAATGAGTGTTCAGCTTTGGGAACTTTGGAATGAATAATT 1378
Db 797 ATTTGCTGTGTTTGTAGCAGAAATGAGTGTTCAGCTTTGGGAACTTTGGAATGAATAATT 856

Qy 1379 AGTAATGGTAATGCTCCATTTA 1400

Db 857 AATAATGGGAATGCTCCANTTA 878

RESULT 14
AAI61293
ID AAI61293 standard; cDNA; 814 BP.
XX AAI61293;
AC AAI61293;
XX 22-OCT-2001 (first entry)
XX Human polynucleotide SEQ. ID NO 5282.
DE Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX Homo sapiens.
OS WO200153312-A1.
PN 26-JUL-2001.
PD 26-DEC-2000; 2000WO-US34263.
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX WPI; 2001-442253/47.
DR P-PSDB; AAM42137.
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX Claim 1; SEQ ID NO 5282; 10078pp; English.
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.M.S disorders
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX SQ Sequence: 814 BP; 263 A; 166 C; 143 G; 242 T; 0 other;
Query Match 32.08; Score 785.6; DB 22; Length 814;
Best Local Similarity 98.88; Pred. No. 4.7e-155;

[illegible]

EPL074617-A2.

07-FEB-2001.

28-JUL-2000; 2000EP-0116126.

29-JUL-1999; 99JP-0248036.

27-AUG-1999; 99JP-0300253.

11-JAN-2000; 2000JP-0118776.

02-MAY-2000; 2000JP-0183767.

09-JUN-2000; 2000JP-0241899.

(HELI-) HELIX RES INST.

Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -

Claim 1; SEQ ID 16124; 2537pp + CD ROM; English.

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13632 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95993 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

Sequence 854 BP; 281 A; 166 C; 162 G; 242 T; 3 other;

Query Match 31.6%; Score 774.8; DB 22; Length 854;
Best Local Similarity 96.9%; Pred. No. 8.8e-153;
Matches: 804; Conservative 0; Mismatches 14; Indels 12; Gaps 1

QY 143 ATAGATAAGTAGTACATGGTGGAATAACTCTACTTTTAGGAGGACTACTCTCTTCGTACA 202
Db 1 ATAGATAAGTAGTACATGGTGGAATAACTCTACTTTTAGGAGGACTACTCTCTTCGTACA 60

QY 203 GTCCTAGACTGGTCTTCTACACTTAAGACACCATTGAGGAGTATGCTCCTATTATTCTT 262
Db 61 GTCCTAGACTGGTCTTCTACACTTAAGACACCATTGAGGAGTATGCTCCTATTATTCTT 120

QY 263 GCCTTTGCGTCGCCAACCCCTCTTTTAGCCCTTCACACATCGCACTGAAGAATATGAT 322
Db 121 GCCTTTGCGTCGCCAACCCCTCTTTTAGCCCTTCACACATCGCACTGAAGAATATGAT 180

QY 323 GCTGAAGGATATGGAAGACACA-----GATGATGATGATGATGATGATGATGATGATGATGA 370
Db 181 GCTGAAGGATATGGAAGACACAGATGATCATGATGATGATGATGATGATGATGATGATGA 240

QY 371 TGATGATGATGATGAGGCACACTCTCTTTTCCACACAGAGCCACGAAGCCATTTTTT 430

Db 241 TGATGATGATGATGAGCAACTCTCTTTTCCACAAGAGAGCCAAAGGCCATTTTTT 300
QY 431 TCCATTTGATCTGTTCCCAATGTGCCATTTGGATGTGCTCTATTCACGAGTTGTACA 490
Db 301 TCCATTTGATCTGTTTCCCAATGTGCCATTTGGATGTGCTCTATTCACGAGTTGTACA 360
QY 491 TTGCTCAGATTTAGGTTTTCACCTCAGTCCCAACCAACATTCCTATTTGATCTCAGATGCT 550
Db 361 TTGCTCAGATTTAGGTTTTCACCTCAGTCCCAACCAACATTCCTATTTGATCTCAGATGCT 420
QY 551 TGATCTTCCAAAACAATAAATAAAGAAATCAAGAAATGATTTTAAAGGACTCACTTC 610
Db 421 TGATCTTCCAAAACAATAAATAAAGAAATCAAGAAATGATTTTAAAGGACTCACTTC 480
QY 611 ACTTTATGCTGATCCTGAAACAACAAGCTAAGGAAAGATTCACCCAAAAGCCCTTCT 670
Db 481 ACTTTATGCTGATCCTGAAACAACAAGCTAAGGAAAGATTCACCCAAAAGCCCTTCT 540
QY 671 AACCACAAAGAAGTTGCGAAGGCTGTATCTGTCCCAACATCAACTAAGTGAATACCCT 730
Db 541 AACCACAAAGAAGTTGCGAAGGCTGTATCTGTCCCAACATCAACTAAGTGAATACCCT 600
LW 731 TAATCTTCCAAAACAATAAATAAAGAAATCAAGAAATGATTTTAAAGAAATACA 790
601 TAATCTTCCAAAACAATAAATAAAGAAATCAAGAAATGATTTTAAAGAAATACA 660
QY 791 AAAGGACACATTCAAAGGAATGAATGCTTTACACGTTTGGAAATGAGTGCAACCCCTCT 850
Db 661 AAAGGACACATTCAAAGGAATGAATGCTTTACACGTTTGGAAATGAGTGCAACCCCTCT 720
QY 851 TGATAATAATGGGATAGAGCCAGGGGCATTTGAAGGGTGACGGTGTCCATATCAGAAAT 910
Db 721 TGATAATAATGGGATAGAGCCAGGGGCATTTGAAGGGTGACGGTGTCCATATCAGAAAT 780
QY 911 TGCAGAAGCAAAACTGACCTCAGTTCTTAAAGGCTTTACCCACCAACTTTAT 960
Db 781 TGCAGAAGCAAAACTGAGNCTCAGTTCTTAAAGATAATCTTCCTTCATTCT 830

Search completed: May 31, 2003, 10:54:25
Job time : 563 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2003, 10:30:17 ; Search time 3450 Seconds

(without alignments)

11519.920 Million cell updates/sec

Title: US-09-944-884-1

Perfect score: 2454

Sequence: 1 ggactaatctggggagcag.....taaaaattgtttgaaat 2454

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

arched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em.estba:*

2: em.esthum:*

3: em.estin:*

4: em.estmu:*

5: em.estov:*

6: em.estpl:*

7: em.estro:*

8: em.htc:*

9: gb.est1:*

10: gb.est2:*

11: gb.htc:*

12: gb.est3:*

13: gb.est4:*

14: gb.est5:*

15: em.estfun:*

16: em.estom:*

17: gb.gss:*

18: em.gss.hum:*

19: em.gss.inv:*

20: em.gss.pln:*

21: em.gss.vrt:*

22: em.gss.fun:*

23: em.gss.mam:*

24: em.gss.mus:*

25: em.gss.other:*

26: em.gss.pro:*

27: em.gss.rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1134.8	46.2	2302	11 AK014504	AK014504 Mus muscu
C 2	665.8	27.1	695	14 BQ004507	BQ004507 UT-H-E10-
C 3	656.4	26.7	672	14 BM992531	BM992531 UT-H-DT0-
4	612.4	25.0	695	10 AW608047	AW608047 RC3-LT002
C 5	608	24.8	626	14 BQ574173	BQ574173 UT-H-E21-
6	587.8	24.0	592	9 AL600795	AL600795 DKEZp313E

7	585.2	23.8	926	14 BQ960688	BQ960688 AGENCOURT
8	579.6	23.6	632	10 AW961537	AW961537 EST373609
C 9	555	22.6	568	10 AW450923	AW450923 UT-H-BI3-
C 10	553.4	22.6	560	12 BF056897	BF056897 7K11G05.X
11	553	22.5	553	9 AL598934	AL598934 DKEZp313F
12	550.4	22.4	591	10 AW955638	AW955638 EST367708
13	527.4	21.5	529	9 AL135736	AL135736 DKEZp5860
C 14	522.4	21.3	533	10 AW192703	AW192703 x150a04.X
C 15	520.4	21.2	603	11 BC022059	BC022059 Homo sapi
C 16	512	20.9	517	12 BF056951	BF056951 7K12D05.X
C 17	511	20.8	517	9 AI655462	AI655462 tt13a07.X
C 18	505.4	20.6	510	10 AW337165	AW337165 xw81906.X
C 19	502.4	20.5	522	13 BM666200	BM666200 UT-E-DX1-
C 20	496	20.2	501	10 AW193820	AW193820 xm30f10.X
C 21	493	20.1	525	9 AI741321	AI741321 w920c02.X
C 22	486.6	19.8	641	10 BE374603	BE374603 60125391
C 23	482.4	19.7	497	10 AW338706	AW338706 ha64d03.X
C 24	477.4	19.5	482	12 BF108809	BF108809 7164d06.X
C 25	473.4	19.3	492	9 AL135737	AL135737 DKEZp5860
C 26	473	19.3	480	9 AI657039	AI657039 tt49d03.X
C 27	472.8	19.3	488	9 AI088424	AI088424 qbl7b10.X
C 28	471	19.2	473	9 AI493987	AI493987 q257e03.X
C 29	470.2	19.2	571	12 BG564080	BG564080 602586130
C 30	470	19.2	471	9 AI862037	AI862037 tw71a05.X
C 31	468	19.1	468	9 AI240315	AI240315 q114c02.X
C 32	467	19.0	491	10 BE049606	BE049606 xw91b10.X
C 33	465.4	19.0	477	9 AI148466	AI148466 qc39e12.X
C 34	464.8	18.9	469	10 AW237808	AW237808 xm81d12.X
C 35	462	18.8	496	9 AI539334	AI539334 te45g09.X
C 36	451.4	18.4	459	9 AI370866	AI370866 ta63h10.X
C 37	450.2	18.3	485	9 AI373846	AI373846 qz96a11.X
C 38	449.8	18.3	462	9 AI277357	AI277357 qm54b03.X
C 39	431.8	17.6	568	9 AI006670	AI006670 ue16b10.Y
C 40	424.4	17.3	476	12 BF823520	BF823520 MRI-RF003
C 41	424	17.3	429	10 AW002412	AW002412 wu61f07.X
C 42	422	17.2	480	9 AA330080	AA330080 EST33760
C 43	418	17.0	559	10 BE633222	BE633222 uv74d03.Y
C 44	415.4	16.9	418	14 N67239	N67239 yz48h02.s1
C 45	412.2	16.8	480	12 BF823517	BF823517 MRI-RF003

ALIGNMENTS

RESULT 1

AK014504

LOCUS

DEFINITION

Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4631401G09:asporin, full insert sequence.

ACCESSION

AK014504

VERSION

AK014504.1 GI:12852406

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (strain:C57BL/6J) 0 day neonate skin cDNA to mRNA, clone.lib:RIKEN full-length enriched mouse cDNA library

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

PUBLISHED

99279253

10349636

REFERENCE

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

PUBLISHED

11042159

REFERENCE

3

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 JOURNAL Tumor Gene Index
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: rcgaps-femail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES Location/Qualifiers
 source 1..695
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="NCI_CGAP_E10"
 /tissue_type="Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)
 with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
 NCI CGAP_E10 is a cDNA library containing the following
 tissue(s): Chondrosarcoma. The library was constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pT73-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is ACACCTGCAC.
 TAG_LIB=UI-H-E10
 TAG_TISSUE=chondrosarcoma
 TAG_SEQ=ACACTTGCAC"

BASE COUNT 240 a 100 c 104 g 251 t
 ORIGIN

Query Match 27.1%; Score 665.8; DB 14; Length 695;
 Best Local Similarity 99.6%; Pred. No. 3.6e-118;
 Matches 678; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1775 CAGAAATTAACAAGACAGTAATGGAAGAGTGCATTACACTATTCTTATTCTTTAGTAAC 1834
 Db 695 CAGAAATTAACAAGACAGTAATGGAAGAGTGCATTACACTATTCTTATTCTTTAGTAAC 636

QY 1835 TTGGGTAGTACTCTAATATTTTAAATCATCTTAAAGTATGATTTGATATATCTTATTGA 1894
 Db 635 TTGGGTAGTACTCTAATATTTTAAATCATCTTAAAGTATGATTTGATATATCTTATTGA 576

QY 1895 AATTACCTTATCATGCTTTAGAGCCGCTCTTTATGTTTAAACATAATTTCTTAAATAAAA 1954
 Db 575 AATTACCTTATCATGCTTTAGAGCCGCTCTTTATGTTTAAACATAATTTCTTAAATAAAA 516

QY 1955 GCCTCAGTAAATGTTCAATACCACCTTGATAAATGCTACTCATAGAGCTGTTGGGG 2014
 Db 515 GCCTCAGTAAATGTTCAATACCACCTTGATAAATGCTACTCATAGAGCTGTTGGGG 456

QY 2015 CTATAGCATATGCTTTTTTTTTTTTAAATTAATTAACCTGATTTAAATCTCTGTAAACAG 2074
 Db 455 CTATAGCATATGCTTTTTTTTTTTTAAATTAATTAACCTGATTTAAATCTCTGTAAACAG 396

QY 2075 TGAGTGTGTTTCATAAAATCTGTAACTCGCATTTTAAATGATCGCGCTATTATAAGCTTTTAA 2134
 Db 395 TGAGTGTGTTTCATAAAATCTGTAACTCGCATTTTAAATGATCGCGCTATTATAAGCTTTTAA 336

QY 2135 TAGCATGAAATTTGTTAGGCTATATACATTTGCCACTTCAACTCTCAAGGAATATTTTGA 2194
 Db 335 TAGCATGAAATTTGTTAGGCTATATACATTTGCCACTTCAACTCTCAAGGAATATTTTGA 276

QY 2195 GATATCCCTTTGGAAGACCTTGCTTGAAGAGAGCTTGACACATAACAAATTTACACCAAT 2254
 Db 275 GATATCCCTTTGGAAGACCTTGCTTGAAGAGAGCTTGACACATAACAAATTTACACCAAT 216

QY 2255 TGCTCTTCAATACATCTATGGAGTGAATACCTCTGAGAACACATCTAGTATAACTGAAT 2314
 Db 215 TGCTCTTCAATACATCTATGGAGTGAATACCTCTGAGAACACATCTAGTATAACTGAAT 156

QY 2315 AACGACAGATCAATTAACACAGACAGAACCCGAAAGCTCTATATAAATGCTCAGAGTTC 2374
 Db 155 AACGACAGATCAATTAACACAGACAGAACCCGAAAGCTCTATATAAATGCTCAGAGTTC 96

QY 2375 TTTATGTAATTTCTTATTGGCATTCAACATATGTATAAATCAGAAAA-CAGGGAAAAATTTTCA 2433
 Db 95 TTTATGTAATTTCTTATTGGCATTCAACATATGTATAAATCAGAAAAACAGGAAATTTTCA 36

QY 2434 TTAATAATATTGTTTGAAT 2454
 Db 35 TTAATAATATTGTTTGAAT 15

RESULT 3
 BM992531/c
 LOCUS
 DEFINITION UI-H-DT0-att-k-09-0-UI.s1 NCI_CGAP_DT0 Homo sapiens cDNA clone
 IMAGE:5864192 3', mRNA sequence.
 ACCESSION BM992531
 VERSION 1 GI:19711920
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 672)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: rcgaps-femail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES Location/Qualifiers
 source 1..672
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="NCI_CGAP_DT0"
 /tissue_type="Metastatic Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia), with a
 modified polylinker; Site_1: EcoR I; Site_2: Not I;
 NCI_CGAP_DT0 is a cDNA library containing the following
 tissue(s): Metastatic Chondrosarcoma in Lung. The library
 was constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into pT73-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 AACTGTTCGG.
 TAG_LIB=UI-H-DT0
 TAG_TISSUE=lung metastatic chondrosarcoma"

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BASE COUNT      235 a      97 c      101 g      239 t
ORIGIN
Query Match      26.7%; Score 656.4; DB 14; Length 672;
Best Local Similarity 99.8%; Pred. No. 2.4e-116;
Matches 657; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1797 GTGAAGAGTGCATTACACATATCTTATCTTTAGTAACCTGGGTAGTACTGTAATATTTT 1856
Db 672 GTGAAGAGTGCATTACACATATCTTATCTTTAGTAACCTGGGTAGTACTGTAATATTTT 613
QY 1857 TAATCATCTTAAAGTATGATTTGATATAATCTTATTGAATTAACCTTATCATGCTTTAGA 1916
Db 612 TAATCATCTTAAAGTATGATTTGATATAATCTTATTGAATTAACCTTATCATGCTTTAGA 553
QY 1917 GCCCGTCTTTTAAACCTTAAATCTTAAATTAAGCCCTTCAGTAATGTTCAATTAC 1976
Db 552 GCCCGTCTTTTAAACCTTAAATCTTAAATTAAGCCCTTCAGTAATGTTCAATTAC 493
QY 1977 CAACCTTGATAATGCTTACTCATAGAGCTGGTTTGGGCTATAGCATATGCTTTTTTTTTT 2036
Db 492 CAACCTTGATAATGCTTACTCATAGAGCTGGTTTGGGCTATAGCATATGCTTTTTTTTTT 433
QY 2037 TTTAATTTATACCTGATTTTAAATCTCTGTAAACCTGTAGTGTTCATATAAATCTGT 2096
Db 432 TTTAATTTATACCTGATTTTAAATCTCTGTAAACCTGTAGTGTTCATATAAATCTGT 373
QY 2097 AACTGCGATTTTAATGATCGGTATTTAAGCTTTTAAAGCTTTAATAGCATGAAATTTGTAGGCTA 2156
Db 372 AACTGCGATTTTAATGATCGGTATTTAAGCTTTTAAAGCTTTTAAAGCATGAAATTTGTAGGCTA 313
QY 2157 TATAACATTTGCCACTTCAACTCTAAGGAATATTTTGGATATATCCCTTTGGAGACCTTG 2216
Db 312 TATAACATTTGCCACTTCAACTCTAAGGAATATTTTGGATATATCCCTTTGGAGACCTTG 253
QY 2217 CTGGAAGAGCTTGGACACTAACAATTTACACCAAAATTTCTCTCAAAATAGCTATGGA 2276
Db 252 CTGGAAGAGCTTGGACACTAACAATTTACACCAAAATTTCTCTCAAAATAGCTATGGA 193
QY 2277 CTGGATACTCTGAGAAACACATCTAGTATATCTGAATTAAGCAGACATCAAAATTAACA 2336
Db 192 CTGGATACTCTGAGAAACACATCTAGTATATCTGAATTAAGCAGACATCAAAATTAACA 133
QY 2337 GACAGAAACCGAAAGCTCTATATAATGCTCAGAGTCTTTTATGATTTCTTTATGGCAT 2396
Db 132 GACAGAAACCGAAAGCTCTATATAATGCTCAGAGTCTTTTATGATTTCTTTATGGCAT 73
QY 2397 TCAACATATGTAATAATCAGAAACAGGAAATTTTCATTAATAATATTTGGTTGAAAT 2454
Db 72 TCAACATATGTAATAATCAGAAACAGGAAATTTTCATTAATAATATTTGGTTGAAAT 15

RESULT 4
LOCUS      AW608047
DEFINITION RC3-LT0023-200100-012-c10 LT0023 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW608047
VERSION     AW608047.1 GI:7312788
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 695)
AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
TITLE     The FAPESP/LICR Human Cancer Genome Project
JOURNAL   Unpublished (1999)
COMMENT   Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
```

```
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-LT0023-200100-012-c10&t3=2000-01-20&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence stop: 634.
Location/Qualifiers
    source          1..695
    organism="Homo sapiens"
    db_xref="taxon:9606"
    clone_lib="LT0023"
    dev_stage="Adult"
    note="Organ: telomios; Vector: puc18; Site: SmaI;
    Site: SmaI; A mini-library was made by cloning products
    derived from ORESTES PCR (U.S. Letters Patent application
    No. 196.716 - Ludwig Institute for Cancer Research)
    profiles into the puc 18 vector. Reverse transcription of
    tissue mRNA and cDNA amplification were performed under
    low stringency conditions."
    BASE COUNT      265 a      138 c      122 g      170 t
    ORIGIN
Query Match      25.0%; Score 612.4; DB 10; Length 695;
Best Local Similarity 95.9%; Pred. No. 6.8e-108;
Matches 639; Conservative 0; Mismatches 26; Indels 1; Gaps 1;
QY 471 TGTATTACGAGTGTGTACATTTGCTCAGATTTAGTGTTCACCTTCAGTCCCAACCAAT 530
Db 6 TGTATTACGAGTGTGTACATTTGCTCAGATTTAGTGTTCACCTTCAGTCCCAACCAAT 65
QY 531 CCATTTGATCTGCAATGCTTGCATCTTCAAAACAATAAATTAAGAAATCAAGAAAT 590
Db 66 CCATTTGATCTGCAATGCTTGCATCTTCAAAACAATAAATTAAGAAATCAAGAAAT 125
QY 591 GATTTTAAAGGACTCACTTTCATTTATGCTGTATCTGATCCTGAACAACAAGCTTAAGCAAG 650
Db 126 GATCTCAAGGACTCACTTTCATTTATGCTGTATCTGATCCTGAACAACAAGCTTAAGCAAG 185
QY 651 ATTCAACCCAAAAGCCCTTCTTAACCAAAAAGAGTTGCGAAGGCTGTATCTGTCCCAAT 710
Db 186 ATTCAACCCAAAAGCCCTTCTTAACCAAAAAGAGTTGCGAAGGCTGTATCTGTCCCAAT 245
QY 711 CAACCTAAGTGAATACCACTTATCTTCCCAATCATATTAGCAGAACTCAGAAATTCATGAA 770
Db 246 CAACCTAAGTGAATACCACTTATCTTCCCAATCATATTAGCAGAACTCAGAAATTCATGAA 305
QY 771 AATAAGTTAAGAAATACAAAAGGACATTTCAAAAGGAATGAATGCTTTACACGTTTGT 830
Db 306 AATAAGTTAAGAAATACAAAAGGACATTTCAAAAGGAATGAATGCTTTACACGTTTGT 365
QY 831 GAAATGAGTGAACCCCTCTTGATATAATGGATAGAGCCAGGGGCTTTTGAAGGGGTG 890
Db 366 GAAATGAGTGAACCCCTCTTGATATAATGGATAGAGCCCTTGAAGGGGTG 425
QY 891 ACGGTGTTCCATATATCAGAAATTCAGAAAGCAAACTGCACCTCAGTCTTCTTAAAGGCTTACCA 950
Db 426 ACGGTGTTCCATATATCAGAAATTCAGAAAGCAAACTGCACCTCAGTCTTCTTAAAGGCTTACCA 484
QY 951 CCAACTTTTATGGAGCTTTCACCTTAGATTATATAATAATTTCAACACTGGAATTTGAGGAT 1010
Db 485 CCAACTTTTATGGAGCTTTCACCTTAGATTATATAATAATTTCAACACTGGAATTTGAGGAT 544
QY 1011 TTTAAACGATACAAAGAACTACAAGGCTGGCCCTAGGAACAACAATAATCACAGATATC 1070
Db 545 TTTAAACGATACAAAGAACTACAAGGCTGGCCCTAGGAACAACAATAATCACAGATATC 604
QY 1071 GAAATGGGAGTCTTGCTAACATACACCTGTGAGAGAAATACATTTGGAAACATAATAA 1130
Db 605 GAAATGGGAGTCTTGCTAACATACACCTGTGAGAGAAATACATTTGGAAACATAATAA 664
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QY 1131 CTRAAA 1136
Db 665 AAAAAA 670

RESULT 5
B0574173/c
LOCUS B0574173 626 bp mRNA linear EST 19-JUN-2002
DEFINITION UI-H-EZ1-baz-i-13-0-UI.s1 NCI-CGAP_Ch2 Homo sapiens cDNA clone
UI-H-EZ1-baz-i-13-0-UI 3', mRNA sequence.
B0574173
ACCESSION B0574173.1 GI:21477490
VERSION EST
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 626)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
Orthopedics
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-48, >AT-rich#Low-complexity (matched complement)
Seq.primer: M13 FORWARD
POLYA=Yes.

FEATURES             Location/Qualifiers
     source           1..626
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                     /db_xref="taxon:9606"
                     /clone="UI-H-EZ1-baz-i-13-0-UI"
                     /clone_lib="NCI-CGAP_Ch2"
                     /tissue_type="Chondrosarcoma Grade II"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Organ: Left Pelvis; Vector: p7T3-Pac (Pharmacia)
                     with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI-CGAP_Ch2 is a normalized cDNA library containing the
                     following tissue(s): Chondrosarcoma Grade II. The library
                     was constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dr primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into p7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dr)18 tail. The sequence tag for this library is
                     TGATCACGCT.
     TAG_LIB=UI-H-EZ1
     TAG_TISSUE=grade-2-chondrosarcoma
     TAG_SEQ=ATCTAATATG"

BASE COUNT 215 a 87 c 95 g 229 t
ORIGIN

Query Match 24.8%; Score 608; DB 14; Length 626;
Best Local Similarity 100.0%; Pred. No. 4.9e-107;
Matches 608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1847 GTAATATTTTAAATCATCTTAAAGTATGATGATATATATCTTATTGAAATACCTTATC 1906
Db 626 GTAATATTTTAAATCATCTTAAAGTATGATGATATATATCTTATTGAAATACCTTATC 567
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QY 1907 ATGCTTAGAGCCGCTCTTTATGTTTAAACTAATTTCTTAAATAAAGCCTTCAGTAAA 1966
Db 566 ATGCTTAGAGCCGCTCTTTATGTTTAAACTAATTTCTTAAATAAAGCCTTCAGTAAA 507
QY 1967 TGTTCATTACCAACTTGCATAAATGCTACTCATAGAGCTGGTTTGGGGCTATAGCATATG 2026
Db 506 TGTTCATTACCAACTTGCATAAATGCTACTCATAGAGCTGGTTTGGGGCTATAGCATATG 447
QY 2027 CTTTTTTTTTTTAAATATTATTACCTGATTTTAAANAATCTCTGTAAANAAGCTGTAGTGTTC 2086
Db 446 CTTTTTTTTTTTAAATATTATTACCTGATTTTAAANAATCTCTGTAAANAAGCTGTAGTGTTC 387
QY 2087 TAAATCTGTAACCTGCGCATTTTAAATGATCGCTATTATAAGCTTTTAAATAGCATGAAAT 2146
Db 386 TAAATCTGTAACCTGCGCATTTTAAATGATCGCTATTATAAGCTTTTAAATAGCATGAAAT 327
QY 2147 TGTAGCTATATAACATTCGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTG 2206
Db 326 TGTAGCTATATAACATTCGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTG 267
QY 2207 GAGACCTTCTTGGAGAGCCTGGACACTTAACAAATTTCTACACCAATTTGCTCTTCAAA 2266
Db 266 GAGACCTTCTTGGAGAGCCTGGACACTTAACAAATTTCTACACCAATTTGCTCTTCAAA 207
QY 2267 TACGTATGGACTGGATAACTCTGAGAAACACATCTAGTATAACTGAATAAGCAGAGCATC 2326
Db 206 TACGTATGGACTGGATAACTCTGAGAAACACATCTAGTATAACTGAATAAGCAGAGCATC 147
QY 2327 AAATTAACAGACAGAAACCGAAAGCTCTATATAAATGCTCAGAGTCTTTATGATATTC 2386
Db 146 AAATTAACAGACAGAAACCGAAAGCTCTATATAAATGCTCAGAGTCTTTATGATATTC 87
QY 2387 TTATTGCCATTCAACATATGTAAATCAGAAACAGGGAATTTTCATTAANAATATTGG 2446
Db 86 TTATTGCCATTCAACATATGTAAATCAGAAACAGGGAATTTTCATTAANAATATTGG 27
QY 2447 TTTGAAAT 2454
Db 26 TTTGAAAT 19

RESULT 6
AL600795 592 bp mRNA linear EST 14-AUG-2001
LOCUS DKF2p313E0538_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
DEFINITION DKF2p313E0538 5', mRNA sequence.
ACCESSION AL600795
VERSION AL600795.1 GI:15164301
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 592)
AUTHORS Wambutt, R., Heubner, D., Mewes, W., Weil, B. and Wiemann, S.
TITLE EST (Wambutt, R., Heubner, D., Mewes, H.W., Weil, B. and Wiemann, S.)
JOURNAL Unpublished (1999)
COMMENT Contact: Wambutt R
MIPS Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DKF2p313E0538) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source           1..592
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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Query Match		24.0%		Score 587.8;		DB 9;		Length 592;	
Best Local Similarity		99.7%		Pred. No. 3.8e-103;					
Matches 589;		Conservative 0;		Mismatches 2;		Indels 0;		Gaps 0;	
<pre> /clone="DKFZp313E0538" /clone_lib="313 (synonym: hlcc2)" /dev_stage="adult" /lab_host="DH10B" /notes="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB; CDNA-collection" </pre>									
Qy	115	TTACACAGTCTCTGAGAACATTTTACATTATAGATAAGTAGTACATGTTGGATAACTTCTA	174						
Dd	2	TTGCACAGTCTCTGAGAACATTTACATTATAGATAAGTAGTACATGTTGGATAACTTCTA	61						
Dd	175	CTTTTAGGAGGACTPACTCTCTCTGACAGTCCTAGACTGGTCTTCTACACTPAAGACACCA	234						
Dd	62	CTTTTAGGAGGACTTACTCTCTCTGACAGTCCTAGACTGGTCTTCTACACTPAAGACACCA	121						
Qy	235	TGAAGGAGTATGTGCTCCTATTATTCTCGCTTTGTGCTCTGCGCAACCCCTTCTTTAGCC	294						
Dd	122	TGAAGGAGTATGTGCTCCTATTATTCTCGCTTTGTGCTCTGCGCAACCCCTTCTTTAGCC	181						
Qy	295	CTTCACACATCGCACTCAAGAATATGATGCTGAAGGATATGGAAGACACACAGATGATGATG	354						
Dd	182	CTTCACACATCGCACTCAAGAATATGATGCTGAAGGATATGGAAGACACACAGATGATGATG	241						
Qy	355	ATGATGATGATGATGATGATGATGATGATGAGGACAACTCTCTTTTCCAAACAGAGAGC	414						
Dd	242	ATGATGATGATGATGATGATGATGATGATGAGGACAACTCTCTTTTCCAAACAGAGAGC	301						
Qy	415	CAAGAAAGCCATTTTTCATTTGATCTGTTTCCAAATGTGCCAATTTGGATGTCAGTGCT	474						
Dd	302	CAAGAAAGCCATTTTTCATTTGATCTGTTTCCAAATGTGCCAATTTGGATGTCAGTGCT	361						
Qy	475	ATTCACAGTGTACATTTGCTCAGATTTAGTTTTCAGTCTCCACCAACCAATTCAT	534						
Dd	362	ATTCACAGTGTACATTTGCTCAGATTTAGTTTTCAGTCTCCACCAACCAATTCAT	421						
Qy	535	TTGATACTCGAATGCTTGATCTTCAAAACCAATAAAATTAAGGAATCAAGAAATGATT	594						
Dd	422	TTGATACTCGAATGCTTGATCTTCAAAACCAATAAAATTAAGGAATCAAGAAATGATT	481						
	595	TTAAAGGACTCAGTTCACCTTTATGGTCTGATCCTGAACAACAACAAGCTATACGAATTC	654						
Dd	482	TTAAAGGACTCAGTTCACCTTTATGGTCTGATCCTGAACAACAACAAGCTATACGAATTC	541						
Qy	655	ACCCAAAGGCTTTCTTAACCAAGAAGTTGCGAAGCTGTATCTGTGCC	705						
Dd	542	ACCCAAAGGCTTTCTTAACCAAGAAGTTGCGAAGCTGTATCTGTGCC	592						

[illegible]

CDNA Library Preparation: ResGen, Invitrogen Corp									
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)									
DNA Sequencing by: Agencourt Bioscience Corporation									
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov									
Plate: LLAM13741 row: g column: 13									
High quality sequence stop: 710.									
Location/Qualifiers									
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/clone_lib="NIH_MGC_129"									
/lab_host="DH10B (phage-resistant)"									
/note="Organ: olfactory epithelium; Vector: pCMV-SPORT6.1.cdb; Site.1: EcoRV; Site.2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."									
BASE COUNT 287 a 194 c 171 g 272 t 2 others									
ORIGIN									
Query Match	23.8%	Score 585.2;	DB 14;	Length 926;					
Best Local Similarity	82.1%	Pred. No. 1.le-102;							
Matches 750;	Conservative	0;	Mismatches 120;	Indels 44;	Gaps 5;				
QY	72	TGTTTTTTTCTCTTTAAATGTAATACCTCTCCATCTTTCTCTCTTTACACACTGTCGTGAGA	131						
DB	56	TTTTTCTCTTTCTTTAAATGTAACACTCTTTATTTTCTCTCTTTGAAGAGTCT-TGAGG	114						
QY	132	ACATTTACATTATAGATAAGTAGTACATGGTGGATAACTTCTACTCTTTTAGGAGGACACTACT	191						
DB	115	ATACTTTACATTTGCGAGTTAAAGTAGTACAGGGTGGATAAATTTCTACTTTTGAAGAAAACCTCT	174						
QY	192	CTCTTCTGACAGTCCTAGACTGGTCTTCTACACTTAAGACACCAATGAAGGAGTATGTGCTC	251						
DB	175	CTCCTCTGACA-----AGGCCAGCATGAAGGAGTATGTGATG	211						
QY	252	CTATTATTCCTGGGCTTTGTGCTGCGCAAAACCCCTTTTACCCCTTCCACACATCGCACTG	311						
DB	212	CTACTGCTTTTGGCTGTGCTCTGCCAAACCCCTTTTACCCCTTCCACACAGCACTG	271						
QY	312	AAGAAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATGATGAT	371						
DB	272	AAGAAATATGATGTTGAAGGATATGGAAGACACA-----GATGATGAC	313						
QY	372	GATGATGATGATGAGGACAACTCTCTTTTCCACACAGAGAGCCCAAGAGCCATTTTTTT	431						
DB	314	GATAACGATGATGACGACAACTCTCTTTTCCACGAAAGAGCCAGTGAACCCCTTTTTC	373						
QY	432	CCATTTGATCTGTTTCCAAATGTGTCATTTGGATGTCAGTGCTATTTCACGAGTTGTACAT	491						
DB	374	CCTTTCGATTTGTTTCCAAACATGTCATTTGGTGGCCCAATGTTACTCTCGAGTTGTTTCAC	433						
QY	492	TGCTCAGATTTAGGTTTGACCTCAGTCCCAACCAACATTCCTCATTTGATACTTCGAATGCTT	551						
DB	434	TGCTCTGATCTAGGTCTGACATCGTTTCCAAACCAACATTCCTCATTTGATACTTCGAATGCTT	493						
QY	552	GATCTTCAAAACAATAAATTAAGGAATCAAGAAATGATTTTAAAGGACTCACTTCA	611						
DB	494	GACCTTCAAAATAATAAATCAAGGAAATTAAGGAAATGACTTTTAAAGGACTCACTTCA	553						
QY	612	CTTTATGCTGTATCTGAACAACAACAAGCTTAAGGAAGTTCACCCAAAGCCCTTTCTA	671						
DB	554	CTTTATGCTGTATCTGAACAACAACAAGCTTAAGGAAGTTCACCCAAAGCCCTTTCTA	613						
QY	672	ACCACAAAGAAGTTGCGAAGGCTGTATCTGTCCCAACAATCAACTAAGTGAATACCACTT	731						
DB	614	ACCACAAAGAATTTGAGAAGGCTATATTTATCCCAACAACCAACTAAGTGAATTTCCACTT	673						
QY	732	AATCTTCCCAATCATTTAGCAGAACTCAGAATTCATGAAAAATAAGTTTAAGAAATACAA	791						

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Db 674 AATCTTCCCAATCATTTAGCAGAACTCAGAAATTCATGATAATAGCTTAAGAAGATACAA 733
QY 792 AAGGACACATTCAAAGGATGAATGCTTTACAGCTTTTGGAAATGAGTCAACACCTCTT 851
Db 734 AAGGACAGCTTCAAGGGAATGAATGCTTTACATGTTTGGAAATGAGTCAACACCTCTT 793
QY 852 GATAATAATGGGATAGAGCCAGGGCATTTGAAGGGTGACGGTGTTCATATACAAAT 911
Db 794 GAGAACACGGGATAGA-CCAGGGGCATTTGAAGGGTGACAGTATTCATATCAGATC 852
QY 912 GCAGAGCAAAACTGACCTCAGCTTCTTAAAGGCTTACCACCACTTATTTGGAGCTTAC 971
Db 853 GCTGAAGCAAAACTAACCTCTATCC-AAAGGGCTACCACCACTTGTGCTGAGCTTCAT 911
QY 972 TTAGATTATAATAA 985
Db 912 TTAGATTTTATAA 925

RESULT 8
AW961537
LOCUS EST373609 MAGE resequences, MAGG Homo sapiens cDNA, mRNA sequence.
DEFINITION
AW961537
VERSION AW961537.1 GI:8151221
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 632)
AUTHORS Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt,
I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeaman, T.J. and
Quackenbush, J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 160
Seq primer: Reverse.
FEATURES
Location/Qualifiers
source
1..632
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COUNT 176 a 128 c 123 g 205 t
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Query Match 23.6%; Score 579.6; DB 10; Length 632;
Best Local Similarity 97.3%; Pred. No. 1.4e-101;
Matches 613; Conservative 0; Mismatches 9; Indels 8; Gaps 2;

QY 7 ATCTGTGGGAGCAGTTTATTCAGATATCACCCAGGGTGCAGGCACACACAGGAGTGTG 66
Db 1 ATCTGTGGGAGCAGTTTATTCAGATATCACCCAGGGTGCAGGCACACAGGAGTGTG 60
QY 67 AAGGGTGTGTTTTCTTTTAAATGAATACCTCTCATCTTTTCTTTACACAGTGTG 126
Db 61 AAGGGTGTGTTTTCTTTTAAATGAATACCTCTCATCTTTTCTTTACACAGTGTG 120
QY 127 TCAGAACATTTACATATAGATAGTACGTACATGTTGGATACCTTACTTTTAGAGGA 186
Db 121 TCAGAACATTTACATATAGATAGTACGTACATGTTGGATACCTTACTTTTAGAGGA 180
QY 187 CTACTCTCTTCTGACAGTCTTACACTGGTCTTCTACACTAAAGCACCATGAGGAGTATG 246
Db 181 CTACTCTCTTCTGACAGTCTTACACTGGTCTTCTACACTAAAGCACCATGAGGAGTATG 240
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QY 247 TGTCTCTATTATTCCTGGCTTTGTGCTCTGCCAAACCCCTTCTTAGCCCTTACACATCG 306
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QY 307 CACTGAAGAATATGATGCTGAAGGATATGAAGACACA-----GATGATGATGATG 360
Db 301 CACTGAAGAATATGATGCTGAAGGATATGAAGACACAGATGATGATGATGATG 360
QY 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
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QY 421 GCCATTTTTCCTCATTTGATCTGTTTCCCAATGTCCTATTTGGATGCTAGTCTATTAC 480
Db 421 GCCATTTTTCCTCATTTGATCTGTTTCCCAATGTCCTATTTGGATGCTAGTCTATTAC 480
QY 481 GAGTTGTACATTTGCTCAGATTTAGGTTTGACCTCAGTCCCAACCAACATTTCCATTGATA 540
Db 481 GAGTTGTACATTTGCTCAGATTTAGGTTTGACCTCAGTCCCAACCAACATTTCCATTGATA 540
QY 541 CTCGAATGCTTGATCTTCAAAACAATAAAATTAAGGAATCAAA-AAAAATGATTTTAA 598
Db 541 CTCGAATGCTTGATCTTCAAAACAATAAAATTAAGGAATCAAA-AAAAATGATTTTAA 600
QY 599 AGGACTCACTTCACTTTATGCTGCTGATCCT 628
Db 601 GGGACTCACTTCACTTTATGCTGCTGATCCT 630

RESULT 9
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LOCUS AW450923
DEFINITION UI-H-BI3-all-f-02-0-UI.s1 NCI-CGAP_Sub5 Homo sapiens cDNA clone
IMAGE:2737275 3', mRNA sequence.
ACCESSION AW450923
VERSION AW450923.1 GI:6991699
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 568)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes.
FEATURES
Location/Qualifiers
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1..568
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/lab_host="NCI-CGAP_Sub5"
/note="Vector: pT73D-Pac (Pharmacia)"
polylinker; Site 1: Not 1; Site 2: Eco RI; NCI-CGAP_Sub5
is a subtracted library derived from NCI-CGAP_Sub4. The
NCI-CGAP_Sub5 library had 3 million recombinants. A
single-stranded DNA preparation of NCI-CGAP_Sub4 was used
as a tracer in a subtractive hybridization with a driver
comprising: the IMAGE pool (NCI-CGAP_Kid3 pool 1 LLAM
3334-3337, 3682-3683, 3798-3803 (IMAGE Clonids
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1322376-1323911, 1456008-1456775, 1500552-1502855);
NCI_CGAP_Kid3 pool 1 LLAM 3342,3722-3725, 3776-3778
(IMAGE Clonoids 1323912-1325831, 1471368-1472903,
1492104-1493255); NCI_CGAP_Lu5 pool 1 LLAM 3575-3582,
3851-3854 (IMAGE Clonoids 1414920-1417991, 1520904-1522439
); NCI_CGAP_G4 pool 1 LLAM 3164-3167, 3716-3720,
3733-3735 (IMAGE Clonoids 1257096-1258631, 1469064-1470983,
1475592-1476743); NCI_CGAP_Pr22 pool 1 LLAM 2457-2459,
2758-2759, 3062-3068 (IMAGE Clonoids 985608-986759
, 1101192-1101959, 1217928-1220615); NCI_CGAP_Co10 pool 1
LLAM 2844-2853, 2871-2872 (IMAGE Clonoids 1057416-1061255
, 1144584-1145351). (10% of the driver population), plus a
pool of 3,840 arrayed clones from NCI_CGAP_Sub1 (IMAGE
Clonoids 2708616-2710535) and NCI_CGAP_Sub2 (IMAGE
Clonoids 2710536-2712455) (10% of the driver population
), plus a pool of 11,136 clones from NCI_CGAP_Sub3 (IMAGE
Clonoids 2712456-2723591) (10% of the driver population),
plus a pool of 5,472 clones from NCI_CGAP_Sub4 (IMAGE
Clonoids 2723592-2728969) (70% of the driver population).
Subtraction was performed as previously described (Bonaldo
, Lennon & Soares (1996): Normalization and Subtraction:
Two Approaches To Facilitate Gene Discovery. Genome
Research 6, 791-806
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TAG_TISSUE=Kidney
TAG_SEQ=AATGC"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7.8e-97;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1900 CCTATCATGCTTAGAGCCGCTCTTTATGTTTAAACCTAATTTCTTAAATAAGCCCTT 1959
|||||
DB 568 CCTATCATGCTTAGAGCCGCTCTTTATGTTTAAACCTAATTTCTTAAATAAGCCCTT 509
|||||
QY 1960 CAGTAAATGTTTCATTACCAACTGCTATAAGAGCTGCTGTTGGGCTATA 2019
|||||
DB 508 CAGTAAATGTTTCATTACCAACTGCTATAAGAGCTGCTGTTGGGCTATA 449
|||||
QY 2020 GCATATGCTTTTATTTTAAATTAATACCTGATTTAAATGCTCTGTAAGAGCTGAG 2079
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DB 448 GCATATGCTTTTATTTTAAATTAATACCTGATTTAAATGCTCTGTAAGAGCTGAG 389
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2080 TGTTTCATAAATCTGTAACCTGCAATTTTAAATGATCCGCTATTATTAAGCTTTTAATAGCA 2139
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DB 388 TGTTTCATAAATCTGTAACCTGCAATTTTAAATGATCCGCTATTATTAAGCTTTTAATAGCA 329
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QY 2140 TGAATAATGTTTAGGCTATATAACATTTGCCACTTCAACTCTAAGGAATATTTTGGAGATAT 2199
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DB 328 TGAATAATGTTTAGGCTATATAACATTTGCCACTTCAACTCTAAGGAATATTTTGGAGATAT 269
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QY 2200 CCCTTTGAAGACCTTGCTTGGAGAGCCTTGACACTAACAAATCTACACCAATTTGCT 2259
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DB 268 CCCTTTGAAGACCTTGCTTGGAGAGCCTTGACACTAACAAATCTACACCAATTTGCT 209
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QY 2260 CTTCAATACCTATGGAATGCTGTAACCTGAGAACACATCTAGTATAACTGAATAAGCA 2319
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DB 208 CTTCAATACCTATGGAATGCTGTAACCTGAGAACACATCTAGTATAACTGAATAAGCA 149
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QY 2320 GAGCATCAAAATTAACACAGACAGAACCCGAAAGCTCTATATAAATGCTCAGAGTTCTTTAT 2379
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DB 148 GAGCATCAAAATTAACACAGACAGAACCCGAAAGCTCTATATAAATGCTCAGAGTTCTTTAT 89
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QY 2380 GTATTTCTTATTTGGCATTTCAACATATGTAATAATCAGAAAACAGGGAATTTTTCATPAAAA 2439
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DB 88 GTATTTCTTATTTGGCATTTCAACATATGTAATAATCAGAAAACAGGGAATTTTTCATPAAAA 29
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QY 2440 ATATTTGGTTGAAAT 2454
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DB 28 ATATTTGGTTGAAAT 14
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RESULT 10
BF056897/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 560

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3444128"

/clone_lib="NCI_CGAP_GC6"

/tissue_type="pooled germ cell tumors"

/lab_host="DH10B"

/note="vector: p7T3D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA

from the normalized library NCI_CGAP_GC4 was prepared, and

ss circles were made in vitro. Following HAP purification,

this DNA was used as tracer in a subtractive hybridization

reaction. The driver was PCR-amplified cDNAs from a pool

of 5,000 clones made from the same library (clonoids

1257096-1258631, 1469064-1470983, and 1475592-1476743).

Subtraction by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 190 a 81 c 92 g 197 t

ORIGIN

Query Match 22.6%; Score 553.4; DB 12; Length 560;

Best Local Similarity 99.8%; Pred. No. 1.6e-96;

Matches 554; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1900 CCTATCATGCTTAGAGCCGCTCTTTATGTTTAAACCTAATTTCTTAAATAAGCCCTT 1959

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DB 560 CCTATCATGCTTAGAGCCGCTCTTTATGTTTAAACCTAATTTCTTAAATAAGCCCTT 501

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QY 1960 CAGTAAATGTTTCATTACCAACTTGATAAATGCTACTCATAGAGCTGTTGGGCTATA 2019

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DB 500 CAGTAAATGTTTCATTACCAACTTGATAAATGCTACTCATAGAGCTGTTGGGCTATA 441

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QY 2020 GCATATGCTTTTATTTTAAATTAATACCTGATTTAAATGCTCTGTAAGAGCTGAG 2079

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DB 440 GCATATGCTTTTATTTTAAATTAATACCTGATTTAAATGCTCTGTAAGAGCTGAG 381

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QY 2080 TGTTTCATAAATCTGTAACCTGCAATTTTAAATGATCCGCTATTATTAAGCTTTTAATAGCA 2139

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DB 380 TGTTTCATAAATCTGTAACCTGCAATTTTAAATGATCCGCTATTATTAAGCTTTTAATAGCA 321

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QY 2140 TGAATAATGTTTAGGCTATATAACATTTGCCACTTCAACTCTAAGGAATATTTTGGAGATAT 2199

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Db      320 TGAATAATGTTAGGCTATATATACATTTGCCACTTCACTCACTAAGGAATATTTTAAAGATAT 261
QY      2200 CCCTTTGGAAGACCTTGTCTGGAAGAGCGCTGGACACTACAAATTTCTACACCAAAATGTCT 2259.
Db      260 CTTTGGGAAGACCTTGTCTGGAAGAGCGCTGGACACTACAAATTTCTACACCAAAATGTCT 201
QY      2260 CTTCAATACGTTATGAGCTGGATTAAGTCTGGAAGACACATCTAGTATTAACGAATAAGCA 2319
Db      200 CTTCAATACGTTATGAGCTGGATTAAGTCTGGAAGACACATCTAGTATTAACGAATAAGCA 141
QY      2320 GAGCATCAATTAACAGACAGACAAACCGAAAGCTCTATATAATGCTCAGAGTTCTTTAT 2379
Db      140 GAGCATCAATTAACAGACAGACAAACCGAAAGCTCTATATAATGCTCAGAGTTCTTTAT 81
QY      2380 GTATTTCTTATTTGGCATTCACATATGTAAATCAGAAACAGGGAATTTTCATTAATA 2439
Db      80 GTATTTCTTATTTGGCATTCACATATGTAAATCAGAAACAGGGAATTTTCATTAATA 21
QY      2440 ATATTGGTTTGAAT 2454
Db      20 ATATTGGTTTGAAT 6

      ILT 11
      98934
LOCUS   AL598934          553 bp      mRNA      linear      EST 14-AUG-2001
DEFINITION DKFZp313F1523_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
ACCESSION AL598934
VERSION    AL598934.1 GI:15161625
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE  1. (bases 1 to 553)
AUTHORS    Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
TITLE      EST (Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Wambutt R
MIPS
Am Klopferpitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DKFZp313F1523) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source            1..553
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                        /db_xref="taxon:9606"
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                        /clone_lib="313 (synonym: hlcc2)"
                        /dev_stage="adult"
                        /lab_host="DH10B"
                        /note="Vector: pTriplEx2; Site_1: SfiI; Site_2: SfiI;
                        cDNA-collection"
BASE COUNT  196 a  107 c  96 g  154 t
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Best Local Similarity 100.0%; Pred. No. 1.9e-96;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      286 TCTTTAGCCCTTCACACATCGCACTGGAAGATATGATGCTGAAGGATATGGAAGACACAG 345
Db      1 TCTTTAGCCCTTCACACATCGCACTGGAAGATATGATGCTGAAGGATATGGAAGACACAG 60
QY      346 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 405

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Db      61 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY      406 CAAGAGAGCCCAAGAGCCATTTTTCATTTGATCTCTTTCCATGTTGTCATTTGATTTGAT 465
Db      121 CAAGAGAGCCCAAGAGCCATTTTTCATTTGATCTCTTTCCATGTTGTCATTTGATTTGAT 180
QY      466 GTCAGTGTCTATTTACGAGCTTGTACATTTCTCAGATTTTAGTTTGGACCTTCAGTCCCAACCA 525
Db      181 GTCAGTGTCTATTTACGAGCTTGTACATTTCTCAGATTTTAGTTTGGACCTTCAGTCCCAACCA 240
QY      526 ACATTCCTATTTGATCTCGAATGCTTGTATCTTCAAAACAATAAATTAAGGAAATCAAG 585
Db      241 ACATTCCTATTTGATCTCGAATGCTTGTATCTTCAAAACAATAAATTAAGGAAATCAAG 300
QY      586 AAATGATTTTAAAGGACTCCTTACCTTTTATGTTGCTGATCTCTGAAACAACAAGCTAA 645
Db      301 AAATGATTTTAAAGGACTCCTTACCTTTTATGTTGCTGATCTCTGAAACAACAAGCTAA 360
QY      646 CGAAGATTCACCCAAAAGCCTTCTAACCAACAAGAAGTTGCGAAGGCTGATCTGTCCC 705
Db      361 CGAAGATTCACCCAAAAGCCTTCTAACCAACAAGAAGTTGCGAAGGCTGATCTGTCCC 420
QY      706 ACAATCAACTAAGTGAATACACACTTAATCTTCCAAATCATTAGCAGAACTCAGAATTC 765
Db      421 ACAATCAACTAAGTGAATACACACTTAATCTTCCAAATCATTAGCAGAACTCAGAATTC 480
QY      766 ATGAAATTAAGTTAAGAAATATACAAAAGGACACATTCAAAAGGAATGAATGCTTTACAG 825
Db      481 ATGAAATTAAGTTAAGAAATATACAAAAGGACACATTCAAAAGGAATGAATGCTTTACAG 540
QY      826 TTTTGGAAATGAG 838
Db      541 TTTTGGAAATGAG 553

      RESULT 12
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LOCUS   AW955638          591 bp      mRNA      linear      EST 01-JUN-2000
DEFINITION EST367708 MAGE resequences, MAGD Homo sapiens cDNA, mRNA sequence.
ACCESSION AW955638
VERSION    AW955638.1 GI:8145321
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE  1. (bases 1 to 591)
AUTHORS    Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
            ,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeaman,T.J. and
            Quackenbush,J.
TITLE      Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
JOURNAL    Unpublished (2000)
COMMENT    Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@tigr.org
            Plate: 81
Seq primer: Reverse.
            Location/Qualifiers
            1..591
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone_lib="MAGE resequences, MAGD"
               /note="Vector: pBluescriptSKm"
BASE COUNT  196 a  87 c  79 g  229 t
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Query Match      22.4%; Score 550.4; DB 10; Length 591;
Best Local Similarity 97.8%; Pred. No. 5.9e-96;

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Matches 579; Conservative 0; Mismatches 11; Indels 2; Gaps 2;
QY 1601 CGTACAAATGATCTTACATAAAATCTCATGCTTGACCATTCCTTTCTCTATACAAAAAG 1660
Db 1 CGTACAAATGATCTTACATAAAATCTCATGCTTGACCATTCCTTTCTCTATACAAAAAG 60
QY 1661 TAAGATATTCGGTATTTAAACACTTTGTTATCAAGACACATTTTAAAGAACTGTACTGTA 1720
Db 61 TAAGATATTCGGTATTTAAACACTTTGTTATCAAGACATATTTTAAAGAACTGTACTGTA 120
QY 1721 AATGAATGCTTGACTTAGCAAAATTTGGCTCTTCATTTGCTGTAGAAAAACAGAT 1780
Db 121 AATGAATGCTTGACTTAGCAAAATTTGGCTCTTCATTTGCTGTAGAAAAACAGAT 180
QY 1781 TAACAAGACACTAATGTAAGAGTGCAATACACATATTTCTTTAGTAGTAACCTGGT 1840
Db 181 TAACAAGACACTAATGTAAGAGTGCAATACACATATTTCTTTAGTAGTAACCTGGT 240
1841 AGTACTGTAATATTTTAAATCATCTTAAAGTAATGATTTGATAATATCTTTATGAAATAC 1900
Db 241 AGTACTGTAATATTTTAAATCATCTTAAAGTAATGATTTGATAATATCTTTATGAAATAC 300
QY 1901 CTTATCATGCTCTAGAGCCGCTTTATGTTTAAACACTAATTTCTTAAATAAGCCCTTC 1960
Db 301 CTTATCATGCTCTAGAGCCGCTTTATGTTTAAACACTAATTTCTTAAATAAGCCCTTC 360
QY 1961 AGTAAATGTTCTATACCAACTTGATAAAATGCTACTCATAGAGCTGGTTGGGGCTATAG 2020
Db 361 AGTAAATGTTCTATACCAACTTGATAAAATGCTACTCATAGAGCTGGTTGGGGCTATAG 420
QY 2021 CATATGCTTTTTTTTTTAAATATTTACCTGATTTTAAATAATCTCTGTAAAAACGTTACT 2080
Db 421 CATATGCTTTTTTTTTTAAATATTTACCTGATTTTAAATAATCTCTGTAAAAACGTTACT 479
QY 2081 GTTTCATAAAATCTGTAATCGCATTTTAAATGATCGCTATTTAATAGCTTTTAAATAG-CA 2139
Db 480 GTTTCATAAAATCTGTAATCGCATTTTAAATGATCGCTATTTAATAGCTTTTAAATAGCCT 539
QY 2140 TGAATAATCTTAGGCTATATACATTTGCCACTTCAACTCTCAAGGAATATTTT 2191
Db 540 TGAATAATCTTAGGCTTTTAAATGATCGCTTTTAAATGATCGCTTTTAAAGAAATTTT 591

RESULT 13
AL135736
S
NTION
529 bp mRNA linear EST 25-FEB-2000
DKFp58600417_r1 586 (synonym: hutel) Homo sapiens cDNA clone
AL135736
AL135736.1 GI:6603923
EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
JOURNAL EST (Koehrer, et al.)
COMMENT Unpublished (1999)
Contact: Koehrer K
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.
SI sequence also available.
This clone (DKFp58600417) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers

FEATURES
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/clone="DKFp58600417"
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/tissue_type="uterus"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI/MluI"
BASE COUNT 179 a 88 c 76 g 186 t
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Best Local Similarity 99.8%; Pred. No. 1.6e-91;
Matches 528; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1859 ATCATCTTTAAAGTATGATTTGATATATCTTATTGAAATACCTTATCATGCTCTTAGAGC 1918
Db 1 ATCATCTTTAAAGTATGATTTGATATATCTTATTGAAATACCTTATCATGCTCTTAGAGC 60
QY 1919 CCGTCTTTATGTTTAAAACTAATTTCTTAAAAATAAGCCTTTCAGTAAATGTTTCATTACCA 1978
Db 61 CCGTCTTTATGTTTAAAACTAATTTCTTAAAAATAAGCCTTTCAGTAAATGTTTCATTACCA 120
QY 1979 ACTTGATTAATGCTACTCATAGAGCTGGTTGGGGCTATAGCATATGCTTTTTTTTTTTT 2038
Db 121 ACTTGATTAATGCTACTCATAGAGCTGGTTGGGGCTATAGCATATGCTTTTTTTTTTTT 180
QY 2039 TAATTATTACCTGATTTTAAAAATCTCTGTAAAAACGCTGTAGTGTTCATAAATCTGTAA 2098
Db 181 TAATTATTACCTGATTTTAAAAATCTCTGTAAAAACGCTGTAGTGTTCATAAATCTGTAA 240
QY 2099 CTCGCATTTTAATGATCGCTATTATTAAGCTTTTAAATAGCATGAAATGTTTAGGCTATA 2158
Db 241 CTCGCATTTTAATGATCGCTATTATTAAGCTTTTAAATAGCATGAAATGTTTAGGCTATA 300
QY 2159 TAACATTCGCACCTTCAACTCTAAGGAATATTTTGAATATCCCTTTGGAAGACCTTGCT 2218
Db 301 TAACATTCGCACCTTCAACTCTAAGGAATATTTTGAATATCCCTTTGGAAGACCTTGCT 360
QY 2219 TGAAGAGCTCGACACTAACAATTTCTACACAAATTTGCTCTTCAATACGTATGGACT 2278
Db 361 TGAAGAGCTCGACACTAACAATTTCTACACAAATTTGCTCTTCAATACGTATGGACT 420
QY 2279 GGATAACTCTGAGAACAACATCTAGTATAAATCTGAATAAGCAGCATCAATTAACACA 2338
Db 421 GGATAACTCTGAGAACAACATCTAGTATAAATCTGAATAAGCAGCATCAATTAACACA 480
QY 2339 CAGAAACCGAAAGCTCTATATAAAATGCTCAGAGTTCTTTTATCTATTTCT 2387
Db 481 CAGAAACCGAAAGCTCTATATAAAATGCTCAGAGTTCTTTTATCTATTTCT 529

RESULT 14
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LOCUS
DEFINITION x150a04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2678094 3',
mRNA sequence.
ACCESSION AW192703
VERSION AW192703.1 GI:6471402
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
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DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40UP from Gibco
 High quality sequence stop: 415.
 Location/Qualifiers

FEATURES

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 /db_xref="taxon:9606"
 /clone_image="IMAGE:2678094"
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 /tissue_type="adenocarcinoma"
 /lab_host="DH10B"
 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dn.
 Average insert size 1.72 kb. Life Technologies catalog #:
 11548-013"

BASE COUNT 183 a 78 c 85 g 187 t

ORIGIN

Query Match 21.3%; Score 522.4; DB 10; Length 533;
 Best Local Similarity 99.8%; Pred. No. 1.5e-90;
 Matches 523; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1931 TTAAGACTAATTTCTTAAATTAAGCCTTCAGTAAATGTTCAATACCAACTTGATAATG 1990
 DB 525 TTTAAACTAATTTCTTAAATTAAGCCTTCAGTAAATGTTCAATACCAACTTGATAATG 466
 QY 1991 CTACTCATAAGAGCTGCTTTGGGCTATAGCATATGCTTTTTTTTTTTTAAATATTACCT 2050
 DB 465 CTACTCATAAGAGCTGCTTTGGGCTATAGCATATGCTTTTTTTTTTTTAAATATTACCT 406
 QY 2051 GATTAAAAATCTCTGTAAAAACGCTAGTGTTCATPAAATCTGTAACTCGCATTTTAA 2110
 DB 405 GATTAAAAATCTCTGTAAAAACGCTAGTGTTCATPAAATCTGTAACTCGCATTTTAA 346
 QY 2111 TGATCCGCTATTATAAGCTTTTATACATGAAATTTGTTAGGCTATATACATTTGCCAC 2170
 DB 345 TGATCCGCTATTATAAGCTTTTATACATGAAATTTGTTAGGCTATATACATTTGCCAC 286
 QY 2171 TTCAACTCTAAGGAATATTTTGGAGATATCCCTTTTGAAGACCTTGCTTGAAGAGCCTG 2230
 DB 285 TTCAACTCTAAGGAATATTTTGGAGATATCCCTTTTGAAGACCTTGCTTGAAGAGCCTG 226
 QY 2231 GACACTAACAAATCTACACCAAAATGCTCTTCAAAATACGATGAGCTGGATTAACCTGA 2290
 DB 225 GACACTAACAAATCTACACCAAAATGCTCTTCAAAATACGATGAGCTGGATTAACCTGA 166
 QY 2291 GAAACACATCTAGTATACTGAATAAGCAGCATCAAAATTAACAGACAGAAACCGAAA 2350
 DB 165 GAAACACATCTAGTATACTGAATAAGCAGCATCAAAATTAACAGACAGAAACCGAAA 106
 QY 2351 GCTCTATAAATGCTCAGAGTCTTTATCTATTTCTTATTTGGCATTCACATATGTAAA 2410
 DB 105 GCTCTATAAATGCTCAGAGTCTTTATGTATTTCTTATTTGGCATTCACATATGTAAA 46
 QY 2411 ATCAGAAAACAGGGAATTTTCAATAAAAATATTGGTTGAAAT 2454
 DB 45 ATCAGAAAACAGGGAATTTTCAATAAAAATATTGGTTGAAAT 2

RESULT 15

BC022059
 LOCUS
 DEFINITION Homo sapiens, similar to asporin (LRR class 1), clone
 IMAGE:4714902, mRNA.
 ACCESSION BC022059
 VERSION BC022059.1 GI:18314458
 KEYWORDS HTC.
 SOURCE Homo sapiens.
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 603)
 Strausberg R.
 Direct Submission
 Submitted (22-JAN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK

COMMENT
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadan@systemsbiology.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 38 Row: 0 Column: 2
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis, genomeScan gene prediction
 This clone has the following problem: frame shifted.

FEATURES

Location/Qualifiers
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ORIGIN

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 Best Local Similarity 97.1%; Pred. No. 3.5e-90;
 Matches 573; Conservative 0; Mismatches 11; Indels 6; Gaps 4;
 QY 1 GGACTAATCTGTGGGAGCAGTTTATCCAGTATACCCAGGGTGCAGCCACACGAGACT 60
 DB 16 GGACTAATCTGTGGGAGCAGTTTATCCAGTATACCCAGGGTGCAGCCACACGAGACT 75
 QY 61 GTCTTGAAGGGTG-TTTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTTTACA 119
 DB 76 GTCTTGAAGGGTGTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTTTACA 135
 QY 120 CAGTGTCTGAGAACATTTACATTATAGATAAGTAGTACATGGTGGATACTTCTACTTTT 179
 DB 136 CAGTGTCTGAGAACATTTACATTATAGATAAGTAGTACATGGTGGATACTTCTACTTTT 195
 QY 180 AGGAGGACTACTCTCTCTGACAGTCTTACAGTGGTCTTCTACACTAAGACACCATGAAG 239
 DB 196 AGGAGGACTACTCTCTCTGACAGTCTTACAGTGGTCTTCTACACTAAGACACCATGAAG 255
 QY 240 GAGTATGTCCTCTATATTCTCTGGCTTTGTGCTGCTGCCAAACCTTCTTTAGCCCTTCA 299
 DB 256 GAGTATGTCCTCTATATTCTCT-GCTTTGTGCTGCTGCCAAACCTTCTTTAGCCCTTCA 314
 QY 300 CACATCGCACTGAAGAATATGATGCTGAAGGATATGAAGACACACA---GATGATGATGAT 356
 DB 315 CACATCGCACTGAAGAATATGATGCTGAAGGATATGAAGACACACAGATGATGATGATGAT 374
 QY 357 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 416
 DB 375 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 434
 QY 417 AGAAGCCATTTTTTCCATTTGATCTGTTTCCAAATGTGCTCCATTTGGATGCTGATGCTAT 476


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Db 435 AGAAGCCATTTTTCATTTGATCTGTTTCCAATGTGTCATTTGGATGTCAGTGCTAT 494
Qy 477 TCACGAGTTGTACATTTGCTCAGATTTAGCTTTGACCTCAGTCCCAACCAACATTTCCATTT 536
Db 495 TCACGAGTTGTACATTTGCTCAGATTTAGGTTTGACCTCAGTCCCAACCAACATTTCCA-TT 553
Qy 537 GATACTCGAATGCTTGATCTTCAAAAACAATAAAATTAAGGAATCAAAGA 586
Db 554 GATACTCGAATGCTTGATCTTCAAAAACAATAAAATTAAGGAATCAAAGA 603
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Search completed: May 31, 2003, 13:38:00
Job time : 3455 secs

GenCore version 5:1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2003, 10:41:47 ; Search time 343 Seconds
(without alignments)
9646.904 Million cell updates/sec

Title: US-09-944-884-1
Perfect score: 2454
Sequence: 1 qqactaatctgtqqgagcaq.....taaaaaattqgtttgaaat 2454

Scoring table: IDENTITY_NUC
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searched:      845702 seqs, 674182571 residues
Total number of hits satisfying chosen parameters: 1691404

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Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match 0%
	Maximum Match 100%
	Listing first 45 su

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	Length			
1	2454	100.0	2454	9	US-09-944-403-1	Sequence 1, Appli
2	2454	100.0	2454	9	US-09-944-413-1	Sequence 1, Appli
3	2454	100.0	2454	9	US-09-944-896-1	Sequence 1, Appli
4	2454	100.0	2454	9	US-09-944-944-1	Sequence 1, Appli
5	2454	100.0	2454	9	US-09-944-907-1	Sequence 1, Appli
6	2454	100.0	2454	9	US-09-944-929-1	Sequence 1, Appli
7	2454	100.0	2454	9	US-10-028-072-327	Sequence 327, App
8	2454	100.0	2454	9	US-10-121-049-327	Sequence 327, App
9	2454	100.0	2454	9	US-10-123-904-327	Sequence 327, App
10	2454	100.0	2454	9	US-10-140-470-327	Sequence 327, App
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44	2454	100.0	2454	9	US-10-123-910-327	Sequence 327, App
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ALIGNMENTS

RESULT 1
US-09-944-413-1
; Sequence 1, Application US/09944413

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1  GENERAL INFORMATION:
2  APPLICANT: Baker, Kevin
3  APPLICANT: Botstein, David
4  APPLICANT: Eaton, Dan
5  APPLICANT: Ferrara, Napoleone
6  APPLICANT: Fillvaroff, Ellen
7  APPLICANT: Gerritsen, Mary
8  APPLICANT: Goddard, Audrey
9  APPLICANT: Godowski, Paul
10 APPLICANT: Grimaldi, Christopher
11 APPLICANT: Gurney, Austin
12 APPLICANT: Hillman, Kenneth
13 APPLICANT: Kiljan, Ivar
14 APPLICANT: Napier, Mary
15 APPLICANT: Roy, Margaret
16 APPLICANT: Tumas, Daniel
17 APPLICANT: Wood, William
18 TITLE OF INVENTION: SECRETED AND TRAN
19 TITLE OF INVENTION: ACIDS ENCODING T
20 FILE REFERENCE: P2548P1C1
21 CURRENT APPLICATION NUMBER: US/09/94
22 CURRENT FILING DATE: 2001-09-26
23 PRIOR APPLICATION NUMBER: 09/866.028
24 PRIOR FILING DATE: 2001-05-25
25 PRIOR APPLICATION NUMBER: 60/067.411
26 PRIOR FILING DATE: December 3, 1997
27 PRIOR APPLICATION NUMBER: 60/069.334
28 PRIOR FILING DATE: December 11, 1997
29 PRIOR APPLICATION NUMBER: 60/069335
30 PRIOR FILING DATE: December 11, 1997
31 PRIOR APPLICATION NUMBER: 60/069,278
32 PRIOR FILING DATE: December 11, 1997
33 PRIOR APPLICATION NUMBER: 60/069,425
34 PRIOR FILING DATE: December 12, 1997
35 PRIOR APPLICATION NUMBER: 60/069,696
36 PRIOR FILING DATE: December 16, 1997
37 PRIOR APPLICATION NUMBER: 60/069,694
38 PRIOR FILING DATE: December 16, 1997

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APPLICANT: WOOD, WILLIAM

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QY	1321	TTGGTTGTGTTTTGAGCAGAAATGAGTCTTCAGCTTGGGAACCTTTGGAATGTAATAATTAG	1380
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QY	1441	TCATTTAATAATGCTAGCTATTATATACAAAGCAAAATATCTATTCTCAAGTGGTAAGTCC	1500
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DB	1561	GGGTTGAGAAACAAGCATCTATGCGATTTCTCTTTTTCGGTACAAATGATCTTACATA	1620
QY	1621	AAATCTCATGCTTGACCATTCCCTTCTTCATAACAACAAAAGTAGATATTCGGTATTTAAC	1680
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QY	1861	CATCTTAAAGTATGATTTGATATAATCTTATGAAATTACCTTATCATGCTTTAGAGCCCC	1920
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QY	1921	GTCCTTTATGTTTAAAACTAATTTCTTAAAAATAAGCCCTTCAGTAAATGTTTCATTACCAAC	1980
DB	1921	GTCCTTTATGTTTAAAACTAATTTCTTAAAAATAAGCCCTTCAGTAAATGTTTCATTACCAAC	1980
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DB	2041	ATTATTACCTTGATTTAAAAATCTCTGTAAAAACGCTGTAGTGTTCATAAAAATCTGTAACCT	2100
QY	2101	CGCATTTTAAATGATCCGCTATTATAAGCTTTTTATAGCATGAAATTTGTTAGGCTATATA	2160
DB	2101	CGCATTTTAAATGATCCGCTATTATAAGCTTTTTATAGCATGAAATTTGTTAGGCTATATA	2160
QY	2161	ACATTTGCCACTTCAACTCTTAAGGAATATTTTTAGATATCCCTTTGGAAGACCTTGCTTG	2220
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RESULT 2

US-09-944-403-1

Sequence 1, Application US/09944403
Patent No. US20020165143A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tamas, Daniel
APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,403
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998

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Db	1021	ACAAAGAACTACAAAGCTGGGGCTTAGGAACAACAANAATCACAGATATCGAAAAATGGGA	1080
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Db 1381 TAAATGGTAAATGCTCCATTTAAATATAGATTCAAAATCCCTACATTTGGATACCTGAAC 1440
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Db 1741 AAAATTTGCTCTTTTCATTTGCTGTAGAAAACAGAAATTAACAAGACAGTAATGTA 1800
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Db 1801 AGAGTGCATTAACACTTCTTATCTTTAGTAACTGGGTAGTACTGTAATATTTTAAAT 1860
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Db 1861 CATCTTAAAGTATGATTTGATATAATCTTATTTGAAATACCTTATCATGCTTAGAGCCC 1920
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Db 1921 GTCCTTATCTTTAAACTATTTCTTAAATAAAGCCTTCAGTAAATGTCATTACCAAC 1980
QY 1981 TTGATAAATGCTACTCATAGAGCTGGTTGGGCTATAGCATATGCTTTTTTTTTTTA 2040
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QY 2041 ATTATTACCTGATTTAAATCTCTGTAAACAGTGTAGTGTTCATAAAATCTGTAAT 2100
Db 2041 ATTATTACCTGATTTAAATCTCTGTAAACAGTGTAGTGTTCATAAAATCTGTAAT 2100
QY 2101 CGCATTTTATGATCGCTTATATAGCTTTTAAATAGCAAGAAATGTTAGGCTATATA 2160
Db 2101 CGCATTTTATGATCGCTTATATAGCTTTTAAATAGCAAGAAATGTTAGGCTATATA 2160
QY 2161 ACATTTGCCACTTCAACTCTAAGGAATATTTTCAGATATCCCTTTTGGAGACCTTGGCTG 2220
Db 2161 ACATTTGCCACTTCAACTCTAAGGAATATTTTCAGATATCCCTTTTGGAGACCTTGGCTG 2220
QY 2221 GAAGAGCTTGGACACTTCAAAATTTCTACACCAAAATGCTCTTCAAAATACGATGGAATG 2280
Db 2221 GAAGAGCTTGGACACTTCAAAATTTCTACACCAAAATGCTCTTCAAAATACGATGGAATG 2280
QY 2281 ATAACTCTGAGAAACACATCTAGTAACTGAATAAGCAGAGATCAAAATTAACAGACA 2340
Db 2281 ATAACTCTGAGAAACACATCTAGTAACTGAATAAGCAGAGATCAAAATTAACAGACA 2340
QY 2341 GAAACCGAAGCTCTATATAAATGCTCAGAGTCTTTATGATTTCTTATTGCAATCAA 2400
Db 2341 GAAACCGAAGCTCTATATAAATGCTCAGAGTCTTTATGATTTCTTATTGCAATCAA 2400
QY 2401 CATATGTAATAATCAGAAAAACAGGAAATTTTCATTAATAAATATTTGGTTGAAAT 2454
|||||

Db 2401 CATATGTAATAATCAGAAAAACAGGAAATTTTCATTAATAAATATTTGGTTGAAAT 2454
RESULT 3
US-09-944-896-1
: Sequence 1, Application US/09944896
: Patent No. US20020168715A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kijavlin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/944, 896
: CURRENT FILING DATE: 2001-08-31
: PRIOR APPLICATION NUMBER: 09/866, 028
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/069, 334
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069, 335
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069, 278
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069, 425
: PRIOR FILING DATE: December 12, 1997
: PRIOR APPLICATION NUMBER: 60/069, 696
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069, 694
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069, 702
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069, 870
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/069, 873
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/068, 017
: PRIOR FILING DATE: December 18, 1997
: PRIOR APPLICATION NUMBER: 60/070, 440
: PRIOR FILING DATE: January 5, 1998
: PRIOR APPLICATION NUMBER: 60/074, 086
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/074, 092
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075, 945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112, 850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113, 296
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146, 222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216, 021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218, 517
: PRIOR FILING DATE: December 22, 1998

;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020168715Aember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020168715Aember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 1
;; LENGTH: 2454
;; TYPE: DNA
;; ORGANISM: Homo Sapien

US-09-944-896-1

Query Match 100.0%; Score 2454; DB 9; Length 2454;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGACTAATCTGTGGGAGCAGTATTATCCAGTATCACCCAGGGTGCAGCCACACCCAGGACT 60
DB 1 GGACTAATCTGTGGGAGCAGTATTATCCAGTATCACCCAGGGTGCAGCCACACCCAGGACT 60
QY 61 GTGTGAAGGGTGTCTTTCTTTTAAATGTAATACCTCCTCATCTTTTCTTTCTTACAC 120
DB 61 GTGTGAAGGGTGTCTTTCTTTTAAATGTAATACCTCCTCATCTTTTCTTTCTTACAC 120
QY 121 AGTGTCTGAGAACATTTACATTTATAGATAGTAGTACATGGTGGATAACTTCTACTTTTA 180
DB 121 AGTGTCTGAGAACATTTACATTTATAGATAGTAGTACATGGTGGATAACTTCTACTTTTA 180
QY 181 GGAGGACTACTCTCTCTGACAGTCTAGACTGGTCTTCTACACTAAGACACCATGAAGG 240
DB 181 GGAGGACTACTCTCTCTGACAGTCTAGACTGGTCTTCTACACTAAGACACCATGAAGG 240
QY 241 AGTATGTCCTCTATTATTCCTGGCTTGTGCTCTGCCAAACCTTCTTTAGCCCTTCAC 300
DB 241 AGTATGTCCTCTATTATTCCTGGCTTGTGCTCTGCCAAACCTTCTTTAGCCCTTCAC 300
QY 301 ACATCGCACTGAGATATGATGCTCTGAGGATATGAAGACACAGATGATGATGATG 360
DB 301 ACATCGCACTGAGATATGATGCTCTGAGGATATGAAGACACAGATGATGATGATG 360
QY 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
DB 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 421 GCCATTTTTCATTTGATCTCTTTCCCAATGTGTCATTTGGATGTCAGTCTATTTCAC 480
DB 421 GCCATTTTTCATTTGATCTCTTTCCCAATGTGTCATTTGGATGTCAGTCTATTTCAC 480

QY 481 GAGTTGTACATTTGCTCAGATTTAGTTTGGACCTCAGTCCCAACCAACATTTCCATTGATA 540
DB 481 GAGTTGTACATTTGCTCAGATTTAGTTTGGACCTCAGTCCCAACCAACATTTCCATTGATA 540
QY 541 CTCGAATGCTTGATCTTTCAAAACAATAAATAAAGGAAATCAAGAAATGATTTTAAAG 600
DB 541 CTCGAATGCTTGATCTTTCAAAACAATAAATAAAGGAAATCAAGAAATGATTTTAAAG 600
QY 601 GACTCATTCTCATTATTTATGGTCTGATCTGAACAACAACAAGCTAACGAAGATTCACCAA 660
DB 601 GACTCATTCTCATTATTTATGGTCTGATCTGAACAACAACAAGCTAACGAAGATTCACCAA 660
QY 661 AAGCCTTTCTAAACCACAAAGAGTTGCGAAGGCTGTATCTGTCCCAACAATCAACTAAGTG 720
DB 661 AAGCCTTTCTAAACCACAAAGAGTTGCGAAGGCTGTATCTGTCCCAACAATCAACTAAGTG 720
QY 721 AAATACCACTTAATCTTTCCCAAAATCATTTAGCAGAACTCAGAAATTCATGAAATAAAGTTA 780
DB 721 AAATACCACTTAATCTTTCCCAAAATCATTTAGCAGAACTCAGAAATTCATGAAATAAAGTTA 780
QY 781 AGAAATACAAAGGACACATTTCAAAGGAATGAATGCTTTTACAGCTTTTGGAAATGAGTG 840
DB 781 AGAAATACAAAGGACACATTTCAAAGGAATGAATGCTTTTACAGCTTTTGGAAATGAGTG 840
QY 841 CAAACCTCTTTGATAATAATGGGATAGAGCCAGGGCATTTGAAGGGGTGACGGTGTTC 900
DB 841 CAAACCTCTTTGATAATAATGGGATAGAGCCAGGGCATTTGAAGGGGTGACGGTGTTC 900
QY 901 ATATCAGATTGCAAGAACAAAACCTGACCTCAGTTCTTAAAGGCTTACCACCACTTTAT 960
DB 901 ATATCAGATTGCAAGAACAAAACCTGACCTCAGTTCTTAAAGGCTTACCACCACTTTAT 960
QY 961 TGGAGCTTCACTTAGATTATAATAAATTTCAACAGTGGAACTTTGAGGATTTTAAAGCAT 1020
DB 961 TGGAGCTTCACTTAGATTATAATAAATTTCAACAGTGGAACTTTGAGGATTTTAAAGCAT 1020
QY 1021 ACRAAGAACTACRAAGGCTGGCCCTAGGAACACAAATACACAGATATCGAAATGGA 1080
DB 1021 ACRAAGAACTACRAAGGCTGGCCCTAGGAACACAAATACACAGATATCGAAATGGA 1080
QY 1081 GTCTTGCTAATACATACCAGTGTGAGAAATATACATTTTGGAAACAAATAAATAAATAA 1140
DB 1081 GTCTTGCTAATACATACCAGTGTGAGAAATATACATTTTGGAAACAAATAAATAAATAA 1140
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DB 1141 TCCCTTCAGGATTTACCAGAGTTGAAATACCTCCAGATAATCTTCCCTTCATTTCAATTCAA 1200
QY 1201 TTGCAAGAGTGGGAGTAATACATTTCTGTCACAGTCCCAAGATGAAGAAATCTTTAT 1260
DB 1201 TTGCAAGAGTGGGAGTAATACATTTCTGTCACAGTCCCAAGATGAAGAAATCTTTAT 1260
QY 1261 ACAGTCAATTAAGTTTATTTCAACAAACCCGGTGAATATCTGGGAAATGCAACCTGCAACAT 1320
DB 1261 ACAGTCAATTAAGTTTATTTCAACAAACCCGGTGAATATCTGGGAAATGCAACCTGCAACAT 1320
QY 1321 TTGCTTGTGTTTGGAGCAGAAATGATGTTGAGCTTTGGGAACTTTGGAATGTAATAATTAG 1380
DB 1321 TTGCTTGTGTTTGGAGCAGAAATGATGTTGAGCTTTGGGAACTTTGGAATGTAATAATTAG 1380
QY 1381 TAATTTGCTTAATGCTCAATTTAATAAGATTCARAAATCCCTACATTTTGGAAATCTTCAAC 1440
DB 1381 TAATTTGCTTAATGCTCAATTTAATAAGATTCARAAATCCCTACATTTTGGAAATCTTCAAC 1440
QY 1441 TCTATTAAATAGTGTAGTATTATATACAGCAAAATATCTATTCTCAAGTGGTGAAGTCC 1500
DB 1441 TCTATTAAATAGTGTAGTATTATATACAGCAAAATATCTATTCTCAAGTGGTGAAGTCC 1500
QY 1501 ACTGACTTTATTTATGACAAAGAAATTTCAACGGAAATTTGCCAAACTATTGTATACATAAG 1560
DB 1501 ACTGACTTTATTTATGACAAAGAAATTTCAACGGAAATTTGCCAAACTATTGTATACATAAG 1560
QY 1561 GGGTTGAGAGAAACAACATCTATTGAGTTCCTTTTTCGGTACAAATGATCTTACATA 1620

Db	1561	GGGTGAGAGAAACAAGCACTAATGCGAGTTTCCTTTTTCGGTACAAATGATCTTACATA	1620
Qy	1621	AATCTCATGCTTGACCATTCCCTTTCTTCATACAAAAAAGTAAGATATTCGGTATTTAAC	1680
Db	1621	AATCTCATGCTTGACCATTCCCTTTCTTCATACAAAAAAGTAAGATATTCGGTATTTAAC	1680
Qy	1681	ACTTTGTTATCAAGCACATTTTAAAAAGAACTGTACTGTAATGGAACTGCTTGACTTAGC	1740
Db	1681	ACTTTGTTATCAAGCACATTTTAAAAAGAACTGTACTGTAATGGAACTGCTTGACTTAGC	1740
Qy	1741	AAAATTTGCTCCTTTTCATTTGCTGTAGAAAAACAGAAATTAACAAGACAGTAATGTGA	1800
Db	1741	AAAATTTGCTCCTTTTCATTTGCTGTAGAAAAACAGAAATTAACAAGACAGTAATGTGA	1800
Qy	1801	AGAGTGCAATACACTATTTCTTATTTCTTAGTAACCTTGGGTAGTACTGTAATATTTTAAT	1860
Db	1801	AGAGTGCAATACACTATTTCTTATTTCTTAGTAACCTTGGGTAGTACTGTAATATTTTAAT	1860
Qy	1861	CATCTTAAAGTAGATTAATTAATCTTATTAAGAAATACCTTATCATGTCCTTAGAGCCC	1920
Db	1861	CATCTTAAAGTAGATTAATTAATCTTATTAAGAAATACCTTATCATGTCCTTAGAGCCC	1920
Qy	1921	GTCTTTATGTTTAAACATAATTTCTTAAAAATAAAGCCTTCAGTAATGTTTCATTACCAAC	1980
Db	1921	GTCTTTATGTTTAAACATAATTTCTTAAAAATAAAGCCTTCAGTAATGTTTCATTACCAAC	1980
Qy	1981	TTGATAAATGCTACTCATAAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTA	2040
Db	1981	TTGATAAATGCTACTCATAAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTA	2040
Qy	2041	ATTATTAACCTGNTTTAAAAATCTCTGTAAAGACGTGTAGTGTTCATAAAATCTGTAAC	2100
Db	2041	ATTATTAACCTGNTTTAAAAATCTCTGTAAAGACGTGTAGTGTTCATAAAATCTGTAAC	2100
Qy	2101	CGATTTTAAATGATCCGCTATTAATAAGCTTTTAATAGCATGAAATGTTTAGGCTATATA	2160
Db	2101	CGATTTTAAATGATCCGCTATTAATAAGCTTTTAATAGCATGAAATGTTTAGGCTATATA	2160
Qy	2161	ACATTGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGCTTG	2220
Db	2161	ACATTGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGCTTG	2220
Qy	2221	GAAGAGCTGGACACTAACAAATTTCTACACAAATTTGCTCTTCAAAATACGTATGGACTGG	2280
Db	2221	GAAGAGCTGGACACTAACAAATTTCTACACAAATTTGCTCTTCAAAATACGTATGGACTGG	2280
Qy	2281	ATAACTCTGAGAAACACATCTAGTATAAATCTGAGAGTGTCTTTATGATATTTTGGCATTC	2340
Db	2281	ATAACTCTGAGAAACACATCTAGTATAAATCTGAGAGTGTCTTTATGATATTTTGGCATTC	2340
Qy	2341	GAACCCGAAAGCTCTATATAAATGCTCAGAGTGTCTTTATGATATTTTGGCATTC	2400
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Qy	2401	CATATGTAATAATCAGAAACAGGGAATTTTTCATTAAAAATATTTGGTTGGTGAAT	2454
Db	2401	CATATGTAATAATCAGAAACAGGGAATTTTTCATTAAAAATATTTGGTTGGTGAAT	2454

RESULT 4

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US-RESOL-94-944-1
: Sequence 1, Application US/09944944
: Patent No. US20020173463A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fillwaroff, Ellen
: APPLICANT: Geritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul

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1801 AGAGTGCATACACTATTCTTATCTTTAGTAACCTGGGTAGTACTGTATATTTTAAAT 1860
1801 AGAGTGCATACACTATTCTTATCTTTAGTAACCTGGGTAGTACTGTATATTTTAAAT 1860
1861 CATCTAAAGTATGATTGATATATCTTTATTTGAATTAACCTTATCATCTCTAGAGCC 1920
1861 CATCTAAAGTATGATTGATATATCTTTATTTGAATTAACCTTATCATCTCTAGAGCC 1920
1921 GTCTTATCTTTAAACTAATTTCTTTAAATAAAGCCTTCACTAAATGTTCAATTAACCAAC 1980
1921 GTCTTATCTTTAAACTAATTTCTTTAAATAAAGCCTTCACTAAATGTTCAATTAACCAAC 1980
1981 TTGATAAATGCTACTCATAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTA 2040
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2041 ATATATACCTGATTTAAAAATCTGTAAAAACGGTGTAGTGTTCATAAAATCTGTAAT 2100
2041 ATATATACCTGATTTAAAAATCTGTAAAAACGGTGTAGTGTTCATAAAATCTGTAAT 2100
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RESULT 5

US-09-944-907-1
; Sequence 1, Application US/09944907
; Publication No. US20020198147A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944, 907
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866, 028

; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 1
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-907-1

Query Match 100.0%; Score 2454; DB 9; Length 2454;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACTAAATCTGGGAGCAGTTTATCCAGTATACCCAGGGTGCAGGCACACCAAGGACT 60
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Db 61 GTGTTGAAGGGTGTCTTTTCTTTTAAATGTAATACCTCCCTCANTCTTTCTTCTACAC 120
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Db 121 AGTGCTCTGAGAACATTTACATTATAGTAAGTAGTACATGGTGGATACTTCTACTTTTA 180
QY 181 GGAGGACTACTCTCTCTGACAGTCTTACAGTGGTCTTCTACACTAAGACACCATGAAG 240
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QY 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Db 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
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Db 661 AAGCCCTTTCTAACCAACAAAGAGTTCGGAAGGCTGTATCTGTCCTCCCAATCAACTAAGTG 720
QY 721 AAATACCACTTAACTTCTCCAAATCATTAGCAGAACTCAGAATTCATGAAAATAAAGTTA 780
Db 721 AAATACCACTTAACTTCTCCAAATCATTAGCAGAACTCAGAATTCATGAAAATAAAGTTA 780
QY 781 AGAAATACAAAGGACACATTTCAAGGAATGAATGCTTTTACACGTTTTTGGAAATGAGTG 840
Db 781 AGAAATACAAAGGACACATTTCAAGGAATGAATGCTTTTACACGTTTTTGGAAATGAGTG 840
QY 841 CAAACCCCTCTGATATAATGAGTACAGCCAGGGCATTTTGAAGGGGTGACGGTCTCC 900
Db 841 CAAACCCCTCTGATATAATGAGTACAGCCAGGGCATTTTGAAGGGGTGACGGTCTCC 900
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Db 901 ATATCAGAAATGTCAGAGCAAAAGTACCTCAGCTTCTTAAAGGCTTACCACCACTTTAT 960
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Db 1021 ACAAAGAACTTACAAAGGCTGGGCTAGGAAACAACAAATACAGATATCGAAATGGGA 1080
QY 1081 GTCTTCTAACATACCACCTGTGAGAAATACATTTGGAAACAATAAATAAATAAATAA 1140
Db 1081 GTCTTCTAACATACCACCTGTGAGAAATACATTTGGAAACAATAAATAAATAAATAA 1140
QY 1141 TCCCTTCAGGATTTACAGAGTTGAATACCTCAGATATAATCTTCCCTTCATCTTAATCAA 1200
Db 1141 TCCCTTCAGGATTTACAGAGTTGAATACCTCAGATATAATCTTCCCTTCATCTTAATCAA 1200
QY 1201 TTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGGCAAGAGTGAAGAAATCTTTAT 1260
Db 1201 TTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGGCAAGAGTGAAGAAATCTTTAT 1260
QY 1261 ACAGTCAATTAAGTTTATTAACAACCCGGTGAATACTGGGAAATGCAACCTGCAACAT 1320
Db 1261 ACAGTCAATTAAGTTTATTAACAACCCGGTGAATACTGGGAAATGCAACCTGCAACAT 1320
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Db 1321 TTGCTTGTGTTTGGAGCAGAAATGAGTCTTGGAGTGGGAACTTTGGAATGTAATAATTAG 1380
QY 1381 TAATGCTAATGCTTAAATTAAGATTCAAAATCCCTACATTTGGAAATCTTGAAC 1440
Db 1381 TAATGCTAATGCTTAAATTAAGATTCAAAATCCCTACATTTGGAAATCTTGAAC 1440
QY 1441 TCTAATTAATGCTAGTATATATACAAAGCAAAATATCTATCTCAAGTGGTAAGTCC 1500
Db 1441 TCTAATTAATGCTAGTATATATACAAAGCAAAATATCTATCTCAAGTGGTAAGTCC 1500
QY 1501 ACTGACTTATTTATGACAAGAAATTTCAACGGAATTTGGCCAACTATTGATACATAAG 1560
Db 1501 ACTGACTTATTTATGACAAGAAATTTCAACGGAATTTGGCCAACTATTGATACATAAG 1560
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Db 1561 GGGTTGAGAGAAACAAGCATCTATTCAGTTCCTTTTGGCGTACAAATGATCTTACATA 1620
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Db 1621 AATCTCATGCTTGACCATTCCTTTTCTTATACAAAGAAAGTAAGATTTGGGTATTAAAC 1680
QY 1681 ACTTTGTTATCAAGCACTTTTAAAGAACTACTGTAAATGGAATGCTTGACATTAGC 1740
Db 1681 ACTTTGTTATCAAGCACTTTTAAAGAACTACTGTAAATGGAATGCTTGACATTAGC 1740
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Db 1741 AAAAAATGCTCTTTCATTTCTGTTAGAAAAACAAGAAATTAACAAAGACAGTAATGTTGA 1800
QY 1801 AGAGTGCATTAACACTATCTTATCTTTAGTAAGTGGGTAGTACTGTAATATTTTAAAT 1860
Db 1801 AGAGTGCATTAACACTATCTTATCTTTAGTAAGTGGGTAGTACTGTAATATTTTAAAT 1860
QY 1861 CATCTTAAAGATGATTTGATATAATCTTTATGAAATACCTTATCATGCTTTAGAGCCC 1920
Db 1861 CATCTTAAAGATGATTTGATATAATCTTTATGAAATACCTTATCATGCTTTAGAGCCC 1920
QY 1921 GTCTTTATGTTTAAACTAATTTCTTAAATAAAGCCTTCAGTAAATGTTATACCAAC 1980
Db 1921 GTCTTTATGTTTAAACTAATTTCTTAAATAAAGCCTTCAGTAAATGTTATACCAAC 1980
QY 1981 TTGATAAATGCTACTCATAGAGCTGGTTTGGGCTATAGCATATGCTTTTTTTTTTTA 2040

Db 1981 TTGATAAATGCTACTCATAGAGCTGGTTTGGGCTATAGCATATGCTTTTTTTTTT 2040
QY 2041 ATATTACCTGATTTTAAATCTCTGTAAACAGTGTAGTCTGTTCATAAAATCTGTAAC 2100
Db 2041 ATATTACCTGATTTTAAATCTCTGTAAACAGTGTAGTCTGTTCATAAAATCTGTAAC 2100
QY 2101 CGCATTTTAAATGATCGCTTATTATAGCTTTTAAATAGCATGAAATTTGTTAGCTATATA 2160
Db 2101 CGCATTTTAAATGATCGCTTATTATAGCTTTTAAATAGCATGAAATTTGTTAGCTATATA 2160
QY 2161 ACATTGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGCCTG 2220
Db 2161 ACATTGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGCCTG 2220
QY 2221 GAAGACCTTGGACACTTAACAATTTACACCAATTTGTCTCTCAATAGCTATGAGACTGG 2280
Db 2221 GAAGACCTTGGACACTTAACAATTTACACCAATTTGTCTCTCAATAGCTATGAGACTGG 2280
QY 2281 ATAACTCTCAGAAACACATCTAGTATACTGAATAGCAGACATCAAAATTAACAGACA 2340
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QY 2341 GAAACCGAAAGCTCTATATAAATGCTCAGAGTTCTTTATGTATTTCTTATTTGCGCATTC 2400
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QY 2401 CATATGTAATAATCAGAAACAGGGAATTTTCAATTAATAATATTTGTTTGAAT 2454
Db 2401 CATATGTAATAATCAGAAACAGGGAATTTTCAATTAATAATATTTGTTTGAAT 2454

RESULT 6
US-09-944-929-1
; Sequence 1, Application US/09944929
; Publication No. US20020197612A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944, 929
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO: 1
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-929-1

Query Match 100.0%; Score 2454; DB 9; Length 2454;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACTAATCTGTGGGAGCAGTTTATTCAGATATCCAGGCTGCGAGCCACACAGGACT 60
Db 1 GGACTAATCTGTGGGAGCAGTTTATTCAGATATCCAGGCTGCGAGCCACACAGGACT 60

Db 2221 GAAGAGCCTGGACACTAAACAATTCTACACCAAAATGTCTCTTCAAAATAGGTATGCACTGG 2280
QY 2281 ATAACCTCTGAGAAACACATCTAGTATTAAGTAAAGCAGACATCAAAATTAACAGACA 2340
Db 2281 ATAACCTCTGAGAAACACATCTAGTATTAAGTAAAGCAGACATCAAAATTAACAGACA 2340
QY 2341 GAAACCGAAAGCTCTATATAAATGCTACAGAGTTCTTTATGTATTTCTTATTGCGCATTCAA 2400
Db 2341 GAAACCGAAAGCTCTATATAAATGCTACAGAGTTCTTTATGTATTTCTTATTGCGCATTCAA 2400
QY 2401 CATATGTAATAACACAGAAACAGGAAATTTTCATTAATAAATATTTGGTTTGAAT 2454
Db 2401 CATATGTAATAACACAGAAACAGGAAATTTTCATTAATAAATATTTGGTTTGAAT 2454

RESULT 7

US-10-028-072-327
; Sequence 327, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
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; PRIOR FILING DATE: 1998-04-09
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; PRIOR FILING DATE: 1998-04-09

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? PRIOR APPLICATION NUMBER: 60/091519
? PRIOR FILING DATE: 1998-07-02
? PRIOR APPLICATION NUMBER: 60/091982
? PRIOR FILING DATE: 1998-07-07

Query Match      100.0%; Score 2454; DB 9; Length 2454;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACTAATCTGCGGAGCAGTTTATTCAGATATCACCCAGGTCAGCCACACAGGACT 60
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Db 1 GGACTAATCTGCGGAGCAGTTTATTCAGATATCACCCAGGTCAGCCACACAGGACT 60
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QY 61 GTGTTGAAGGGTGTCTTTTCTTTTAAATACCTCCTCATCTTTCTTCTTCTTACAC 120
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Db 61 GTGTTGAAGGGTGTCTTTTCTTTTAAATACCTCCTCATCTTTCTTCTTCTTACAC 120
   |||||
QY 121 AGTGTCTGAGAACATTTACATTAAGTAGTAGTACATGGTGGATPACTTCTACTTTTA 180
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Db 121 AGTGTCTGAGAACATTTACATTAAGTAGTAGTACATGGTGGATPACTTCTACTTTTA 180
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QY 181 GGAGGACTACTCTCTTCTGACAGTCTTCTGACAGTCTTCTGACAGTCTTCTGACAGT 240
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Db 181 GGAGGACTACTCTCTTCTGACAGTCTTCTGACAGTCTTCTGACAGTCTTCTGACAGT 240
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QY 241 AGTATGTCTCTCTTATTTATTCCTGGCTTTGTGCTCTGCCAAACCTTTCTTTAGCCCTTCAC 300
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QY 361 ATGATGATGATGATGATGATGATGAGGACAACTCTCTTTTCCAAACAGAGAGCCCAAGAA 420
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Db 361 ATGATGATGATGATGATGATGATGAGGACAACTCTCTTTTCCAAACAGAGAGCCCAAGAA 420
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QY 421 GCCATTTTCTCCATTTGATCTCTTTCCAAATGTGCTCATTTGGATGCTGATGCTATTTCAC 480
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Db 421 GCCATTTTCTCCATTTGATCTCTTTCCAAATGTGCTCATTTGGATGCTGATGCTATTTCAC 480
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QY 541 CTCGAATGCTTGTATCTTTCAAAACAATAAATAAGGAATCAAGAAATGATTTTAAAG 600
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Db 541 CTCGAATGCTTGTATCTTTCAAAACAATAAATAAGGAATCAAGAAATGATTTTAAAG 600
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QY 601 GACTCACTTCACTTTATGCTGCTGATCTGAAACAACAAGCTTAACGAAGATTCACCCAA 660
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Db 601 GACTCACTTCACTTTATGCTGCTGATCTGAAACAACAAGCTTAACGAAGATTCACCCAA 660
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QY 661 AAGCCTTTCTAACCAACAAGAGTTCGGAAGGCTGTATCTGTCCCAACAATCAACTAAGTG 720
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Db 661 AAGCCTTTCTAACCAACAAGAGTTCGGAAGGCTGTATCTGTCCCAACAATCAACTAAGTG 720
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QY 721 AATACCACTTAATCTTCCCAAAATCATTAGCAGAACTCAGAAATTCATGAATAAAGTTA 780
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Db 721 AATACCACTTAATCTTCCCAAAATCATTAGCAGAACTCAGAAATTCATGAATAAAGTTA 780
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QY 781 AGAAATACAAAAGGACACATTTCAAAGGAATGATGCTTTTACACGTTTTCGAAATGAGTG 840
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QY 841 CAAACCTCTTGATAATAATGGGATAGAGCCAGGGGCAATTTGAAGGGTGACGGTCTCC 900
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QY 901 ATATCAGAATTCAGAGCAAAAACCTGACCTCAGTCTTCTTAAAGGCTTACCAACCACTTAT 960
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Db 901 ATATCAGAATTCAGAGCAAAAACCTGACCTCAGTCTTCTTAAAGGCTTACCAACCACTTAT 960
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QY 961 TGGAGCTTCACTTAGATTATAAATAATTTCAACAGTGGAACTTGAGGATTTTAAACGAT 1020
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QY 1021 ACAAAGAACTACAAAGGCTGGGCTAGGAAACAAACAAATACAGATATCGAAATGGGA 1080
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Db 1021 ACAAGAACTACAAAGGCTGGGCTAGGAAACAAACAAATCACAGATATCGAAATGGGA 1080
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QY ATTATTAACCTGATTTTAAATCTCTTAAAGAGCTGTAGTGTTCATATAAATCTGTAAC 2100
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QY CGCATTTTAAATGATGCGCTATTATAAGCTTTTAAATAGCATGAAATTTGTTAGGCTATATA 2160
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QY CATATGTAATTAATCAGAAACAGGAAATTTTCATTAATAAATATTTGTTGAAAT 2454
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RESULT 8

US-10-121-049-327
; Sequence 327, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121.049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 327
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-121-049-327

Query Match 100.0%; Score 2454; DB 9; Length 2454;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB	301	ACATCCGACTGAAGATATGATGCTCTGAAGGATATGAAGACACAGATGATGATGATGATG	360
QY	361	ATGATGATGATGATGATGATGAGGACAACCTCTCTTTTCCACAAGAGAGGCCAAGAA	420
DB	361	ATGATGATGATGATGATGATGAGGACAACCTCTCTTTTCCACAAGAGAGGCCAAGAA	420
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DB	421	GCCATTTTTTCCATTTGATCTGCTTTTCCAAATGTGTCCATTTGGATGTCAGTCTATTTCAC	480
QY	481	GAGTTGTACATTCCTCAGATTTTAGGTTTGAACCTCAGTCCCAACCAACATTTCCATTTGATA	540
DB	481	GAGTTGTACATTCCTCAGATTTTAGGTTTGAACCTCAGTCCCAACCAACATTTCCATTTGATA	540
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DB	541	CTCGAATGCTTGATCTTCCAAACAATAAAATTAAAGGAAATCAAAGAAAAATGATTTTAAAG	600
QY	601	GACTCAGTCTACATTTATGGTCTGATCGTGAACAACAACAGCTTAACGAAGATTCACCCAA	660
DB	601	GACTCAGTCTACATTTATGGTCTGATCGTGAACAACAACAGCTTAACGAAGATTCACCCAA	660
QY	661	AAGCCTTCTTAACCAACAAGAAGTTCGGAAGGCTGTATCTGTCCCACAATCAACTAAGTG	720
DB	661	AAGCCTTCTTAACCAACAAGAAGTTCGGAAGGCTGTATCTGTCCCACAATCAACTAAGTG	720
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DB	721	AAATACCACCTTAATCTTCCAAAATCATTTAGCAGAATCTCAGAATTCATGAAAAATAAGTTA	780
QY	781	AGAAAATACAAAAGGACACATTCAAAGGAATGAATGCTTTTACACGTTTTGGAATGAGTG	840
DB	781	AGAAAATACAAAAGGACACATTCAAAGGAATGAATGCTTTTACACGTTTTGGAATGAGTG	840
QY	841	CAAAACCTCTTGATAATAATGGGATAGAGCCAGGGGCATTTGAAGGGGTGACGGTCTTC	900
DB	841	CAAAACCTCTTGATAATAATGGGATAGAGCCAGGGGCATTTGAAGGGGTGACGGTCTTC	900
QY	901	ATATCAGAAATGCGAAGCAAAAATGACCTCAGTCTCTTAAAGGCTTACCAACCACTTTAT	960
DB	901	ATATCAGAAATGCGAAGCAAAAATGACCTCAGTCTCTTAAAGGCTTACCAACCACTTTAT	960
QY	961	TGGAGCTTCACTTTAGATTATAATAAAATTTCAACAGTGGAACTTTGAGGATTTTAAACGAT	1020
DB	961	TGGAGCTTCACTTTAGATTATAATAAAATTTCAACAGTGGAACTTTGAGGATTTTAAACGAT	1020
QY	1021	ACAAAGACTACAAAAGCTGGGCTTAGGAACAACAATAATCACAGATATCGAAAAATGGGA	1080
DB	1021	ACAAAGACTACAAAAGCTGGGCTTAGGAACAACAATAATCACAGATATCGAAAAATGGGA	1080
QY	1081	GTCTTGCTAACATACCACGTTGAGAGAAATACATTTGGAAAAACAATAAACTAAAAAAA	1140
DB	1081	GTCTTGCTAACATACCACGTTGAGAGAAATACATTTGGAAAAACAATAAACTAAAAAAA	1140
QY	1141	TCCTCTCAGGATTTACCAGAGTTGAAATACCTCCAGATAATCTTCCCTTCATCTTAATCAA	1200
DB	1141	TCCTCTCAGGATTTACCAGAGTTGAAATACCTCCAGATAATCTTCCCTTCATCTTAATCAA	1200
QY	1201	TTGCAAGAGTGGGAGTAAATGACTTCTGTCCACAGTGCCAAAGATGAAGAAATCTTTAT	1260
DB	1201	TTGCAAGAGTGGGAGTAAATGACTTCTGTCCACAGTGCCAAAGATGAAGAAATCTTTAT	1260

Qy	1261	ACAGTGCATAAGCTTATTTCACAACCCGGTGAATACTGGGAAATGCAACCTGCAACAT	1320
Db	1261	ACAGTGCATAAGCTTATTTCACAACCCGGTGAATACTGGGAAATGCAACCTGCAACAT	1320
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Db	1321	TTCGTTGTGTGTTTTGAGCAGAATCAGGTGTCAGCTTCGGAACTTTTGGAAATGTAATAATTAG	1380
Qy	1381	TAATTGGTAATGTCCATTTTAATAATAAGATTTCAAAAATCCCTACATTTTGGAAATACTTTGAAC	1440
Db	1381	TAATTGGTAATGTCCATTTTAATAATAAGATTTCAAAAATCCCTACATTTTGGAAATACTTTGAAC	1440
Qy	1441	TCATTAAATAAGTGGTAGTATTATATATACAAAGCAAAATATCTATTCTCAAGTGGTAGTCC	1500
Db	1441	TCATTAAATAAGTGGTAGTATTATATATACAAAGCAAAATATCTATTCTCAAGTGGTAGTCC	1500
Qy	1501	ACTGACCTATTTTATGACAGAATAATTTCAAGCAAACTTTTGCCTCAAACTATTGTATACATAAG	1560
Db	1501	ACTGACCTATTTTATGACAGAATAATTTCAAGCAAACTTTTGCCTCAAACTATTGTATACATAAG	1560
Qy	1561	GGGTTGAGAGAAACAAGCATCTATTGTCAGTTCCTTTTTGCGTACAAATGATCTTACATA	1620
Db	1561	GGGTTGAGAGAAACAAGCATCTATTGTCAGTTCCTTTTTGCGTACAAATGATCTTACATA	1620
Qy	1621	AATCTCATGCTTGACCATTCCTTCTTCTATPACAAAAAGTAAGATTTTCGCTATTTAAC	1680
Db	1621	AATCTCATGCTTGACCATTCCTTCTTCTATPACAAAAAGTAAGATTTTCGCTATTTAAC	1680
Qy	1681	ACTTTGTTATCAGACACATTTTAAAAGAACTCTACTGTAAATGGAACTCTTCACATTAGC	1740
Db	1681	ACTTTGTTATCAGACACATTTTAAAAGAACTCTACTGTAAATGGAACTCTTCACATTAGC	1740
Qy	1741	AAAATTTGCTCTTTTCATTTCGCTGTAGAAAAACAGAAATTAACAAAGACAGTAATGTGA	1800
Db	1741	AAAATTTGCTCTTTTCATTTCGCTGTAGAAAAACAGAAATTAACAAAGACAGTAATGTGA	1800
Qy	1801	AGAGTGCAATPACACTATCTTTATCTTTTAGTAAGTCTGGGTAGTACTGTAATATTTTAAAT	1860
Db	1801	AGAGTGCAATPACACTATCTTTATCTTTTAGTAAGTCTGGGTAGTACTGTAATATTTTAAAT	1860
Qy	1861	CATCTTAAAGTAGATTGTGATATAACTTTATGAAATTACCTTATCATGCTCTTAGAGCCC	1920
Db	1861	CATCTTAAAGTAGATTGTGATATAACTTTATGAAATTACCTTATCATGCTCTTAGAGCCC	1920
Qy	1921	GTCTTTATGTTTAAACATAATTTCTTAAAAATAAGCCCTTCAGTAAATGTTTCATTACCAAC	1980
Db	1921	GTCTTTATGTTTAAACATAATTTCTTAAAAATAAGCCCTTCAGTAAATGTTTCATTACCAAC	1980
Qy	1981	TTGATAAATGCTACTCATAGAGCTGGTTTTGGGCTATAGCATATGCTTTTTTTTTTTTA	2040
Db	1981	TTGATAAATGCTACTCATAGAGCTGGTTTTGGGCTATAGCATATGCTTTTTTTTTTTTA	2040
Qy	2041	ATTATTACCTGATTTAAAAATCTCTGTAAAAACGCTGAGTGTTCATAAAATCTGTAACCT	2100
Db	2041	ATTATTACCTGATTTAAAAATCTCTGTAAAAACGCTGAGTGTTCATAAAATCTGTAACCT	2100
Qy	2101	CGCATTTTAAATGATCCGCTATTATAAGCTTTTAAATAGCATGAAATTTGTTAGGCTATATA	2160
Db	2101	CGCATTTTAAATGATCCGCTATTATAAGCTTTTAAATAGCATGAAATTTGTTAGGCTATATA	2160
Qy	2161	ACATTGGCACTTCAAACTCTAAGGAATATTTTGGATATCCCTTTGGAAGACCTTGTCTTG	2220
Db	2161	ACATTGGCACTTCAAACTCTAAGGAATATTTTGGATATCCCTTTGGAAGACCTTGTCTTG	2220
Qy	2221	GAAGAGCCTTGGACACTAACAAATTTCTACACCAAATTTGTCTCTTCAAAATACGTATGGACTGG	2280
Db	2221	GAAGAGCCTTGGACACTAACAAATTTCTACACCAAATTTGTCTCTTCAAAATACGTATGGACTGG	2280
Qy	2281	ATAACTCTGAGAAACACATCTAGTATAAATGAAATAGCAGAGCATCAAAATTAACAGACA	2340
Db	2281	ATAACTCTGAGAAACACATCTAGTATAAATGAAATAGCAGAGCATCAAAATTAACAGACA	2340
Qy	2341	GAACCCAAAGCTCTATATAAAATCTCTCAGAGTCTCTTTTATCTTATTTTATTTGGCATCAA	2400

Db 601 GACTCACTTACCTTTATGGTCTGATCCTGAACAACAACAGCTAAGCAAGATTTCACCCAA 660
QY 661 AAGCCCTTCTTAACCAACAAGAAAGTTCGGAAGGCTGTATCTGCCCAATCAACTAAGTG 720
Db 661 AAGCCCTTCTTAACCAACAAGAAAGTTCGGAAGGCTGTATCTGCCCAATCAACTAAGTG 720
QY 721 AATATACCACTTAATCTCCCAATCATATTAGCAAGACTCAGAATTCATGAAAAATAAGTTA 780
Db 721 AATATACCACTTAATCTCCCAATCATATTAGCAAGACTCAGAATTCATGAAAAATAAGTTA 780
QY 781 AGAAATACAAAAGGACACATTCAAAGGATGAATGCTTTACAGCTTTTGGAAATGAGTG 840
Db 781 AGAAATACAAAAGGACACATTCAAAGGATGAATGCTTTACAGCTTTTGGAAATGAGTG 840
QY 841 CAAACCCCTCTTGATAATAATGGGATAGACCGGGGCATTGAAGGGGTGACGGGTCTTC 900
Db 841 CAAACCCCTCTTGATAATAATGGGATAGACCGGGGCATTGAAGGGGTGACGGGTCTTC 900
QY 901 ATATCAGAAATTCGAGAAGCAAAACTGACCTCAGTCTCTTAAAGGCTTACCACCAACTTTAT 960
Db 901 ATATCAGAAATTCGAGAAGCAAAACTGACCTCAGTCTCTTAAAGGCTTACCACCAACTTTAT 960
Y 961 TGGAGCTTCACTTAGATTATAATAAATTCACAGTGGAACTTGAGGATTTAAACGAT 1020
Db 961 TGGAGCTTCACTTAGATTATAATAAATTCACAGTGGAACTTGAGGATTTAAACGAT 1020
QY 1021 ACAAGAACTACAAAAGGCTGGGCTAGGAACAACAATAATCACAGATATCGAAAAATGGGA 1080
Db 1021 ACAAGAACTACAAAAGGCTGGGCTAGGAACAACAATAATCACAGATATCGAAAAATGGGA 1080
QY 1081 GTCTTGCTTAACATPACCACGCTGAGAGAAATACATTTGGAAAAACAATAAACTAAAAAAA 1140
Db 1081 GTCTTGCTTAACATPACCACGCTGAGAGAAATACATTTGGAAAAACAATAAACTAAAAAAA 1140
QY 1141 TCCCTTCAGATPACCAGAGTTCGAATACCTCCAGATAATCTTCCTCACTTAATTCAA 1200
Db 1141 TCCCTTCAGATPACCAGAGTTCGAATACCTCCAGATAATCTTCCTCACTTAATTCAA 1200
QY 1201 TTGCAAGAGTGGGAGTAAATGACTTCTGTCACACAGTGCCAAAGATGAAGAAATCTTTAT 1260
Db 1201 TTGCAAGAGTGGGAGTAAATGACTTCTGTCACACAGTGCCAAAGATGAAGAAATCTTTAT 1260
QY 1261 ACAGTGCATTAAGTTTATTCACAAACCCGCTGAAATCTGGGAAATGCAACCTGCAACAT 1320
Db 1261 ACAGTGCATTAAGTTTATTCACAAACCCGCTGAAATCTGGGAAATGCAACCTGCAACAT 1320
QY 1321 TTGCTTGTGTTTGAGCAGATGAGTGTTCAGCTTGGGAATTTGGAAATGTAATAATTAG 1380
Db 1321 TTGCTTGTGTTTGAGCAGATGAGTGTTCAGCTTGGGAATTTGGAAATGTAATAATTAG 1380
QY 1381 TAATTTGTAATGTCCTTAATTAATTAAGATTCAAAAATCCCTACATTTGGAAATCTTGAAC 1440
Db 1381 TAATTTGTAATGTCCTTAATTAATTAAGATTCAAAAATCCCTACATTTGGAAATCTTGAAC 1440
QY 1441 TCTATTAAATGAGTATTAATATATACAAAGCAAAATATCTATTCTCAAGTGGTAAGTCC 1500
Db 1441 TCTATTAAATGAGTATTAATATATACAAAGCAAAATATCTATTCTCAAGTGGTAAGTCC 1500
QY 1501 ACTGACTTATTTATGACAGAAATTTCAACGGAAATTTGCCAAACTATTGATACATAAG 1560
Db 1501 ACTGACTTATTTATGACAGAAATTTCAACGGAAATTTGCCAAACTATTGATACATAAG 1560
QY 1561 GGGTTGAGAAACAAGCATCTATTGCGATTTCTCTTTTTCGCTACAAATGATCTTACATA 1620
Db 1561 GGGTTGAGAAACAAGCATCTATTGCGATTTCTCTTTTTCGCTACAAATGATCTTACATA 1620
QY 1621 AATCTCATGCTTGACCATTCCTTTCTTCATPACAAAAAAGTAAGATATTCGGTATTAAAC 1680
Db 1621 AATCTCATGCTTGACCATTCCTTTCTTCATPACAAAAAAGTAAGATATTCGGTATTAAAC 1680
QY 1681 ACITTTGTTATCAGACACATTTTAAAAAGAACTGCTGTAATGGAATGCTTGACATTAGC 1740
|||||

Db 1681 ACTTTGTTATCAGACACATTTTAAAAAGAACTGCTACTGTGTAATGGAATGCTTGACTTAGC 1740
QY 1741 AAAATTTGCTGCTTTTCATTTGCTTTAGAAAAACAGAAATTAACAAAGACAGATAATGTA 1800
Db 1741 AAAATTTGCTGCTTTTCATTTGCTTTAGAAAAACAGAAATTAACAAAGACAGATAATGTA 1800
QY 1801 AGAGTGCATTAACACTATTCTTTAGTAACTTTGGGTAGTACTGTAATATTTTAAAT 1860
Db 1801 AGAGTGCATTAACACTATTCTTTAGTAACTTTGGGTAGTACTGTAATATTTTAAAT 1860
QY 1861 CATCTTAAAGTATGATTGTGATATAATCTTAAATATACCTTATCATGCTTTAGAGCCC 1920
Db 1861 CATCTTAAAGTATGATTGTGATATAATCTTAAATATACCTTATCATGCTTTAGAGCCC 1920
QY 1921 GTCTTTATGTTTAAAACTAAATTTCTTAAAAATAAGCCCTTCAGTAAATGTTTCATTACCAAC 1980
Db 1921 GTCTTTATGTTTAAAACTAAATTTCTTAAAAATAAGCCCTTCAGTAAATGTTTCATTACCAAC 1980
QY 1981 TTGATAAATGCTACTCATTAAGAGCTGGTTGGGGCTATAGCATATGCTTTTTTTTTTTA 2040
Db 1981 TTGATAAATGCTACTCATTAAGAGCTGGTTGGGGCTATAGCATATGCTTTTTTTTTTTA 2040
QY 2041 ATTATTACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTCATAAAATCTGTAAC 2100
Db 2041 ATTATTACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTCATAAAATCTGTAAC 2100
QY 2101 CGCATTTTAAATGATCGGCTATTATAAGCTTTTAAATAGCATCAAAATTTGTTAGGCTATATA 2160
Db 2101 CGCATTTTAAATGATCGGCTATTATAAGCTTTTAAATAGCATCAAAATTTGTTAGGCTATATA 2160
QY 2161 ACATTCGCTCTCACTCTAAGGAAATATTTTGGAGATATCCCTTTGGAAGACCTTGCTG 2220
Db 2161 ACATTCGCTCTCACTCTAAGGAAATATTTTGGAGATATCCCTTTGGAAGACCTTGCTG 2220
QY 2221 GAAGAGCTGGACACTAAACAATCTACACCAAAATGTCTCTCAAAATACGATGAGCTGG 2280
Db 2221 GAAGAGCTGGACACTAAACAATCTACACCAAAATGTCTCTCAAAATACGATGAGCTGG 2280
QY 2281 ATAACCTGAGAAACACATCTAGTATAACTGAATAAGCAGAGCATCAAAATTAACAGACA 2340
Db 2281 ATAACCTGAGAAACACATCTAGTATAACTGAATAAGCAGAGCATCAAAATTAACAGACA 2340
QY 2341 GAACCGAAAGCTCTATATAAATGCTCAGAGTCTTTTATGTTTATTTGCGATTCAA 2400
Db 2341 GAACCGAAAGCTCTATATAAATGCTCAGAGTCTTTTATGTTTATTTGCGATTCAA 2400
QY 2401 CATATGTAAATCAGAAAAACAGGAAATTTTCATTAATAAATATTTGTTTGAAT 2454
Db 2401 CATATGTAAATCAGAAAAACAGGAAATTTTCATTAATAAATATTTGTTTGAAT 2454

RESULT 11

US-10-175-746-327
; Sequence 327, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin


```
Db 1921 GTCTTTATGTTTAAACCTAATTTCTTAAATTAAGCCCTTCAGTAATGTCATTACCAAC 1980
Qy 1981 TTGATAAATGCTACTCATAAGAGCTGTTTGGGCTATAGCATATGCTTTTATTTT 2040
Db 1981 TTGATAAATGCTACTCATAAGAGCTGTTTGGGCTATAGCATATGCTTTTATTTT 2040
Qy 2041 ATATTACCTGATTTAAATCTCTGTAATAACGCTAGTCTTTTATAGGCTATATA 2100
Db 2041 ATATTACCTGATTTAAATCTCTGTAATAACGCTAGTCTTTTATAGGCTATATA 2100
Qy 2101 CGCATTTTAAATGATCCGCTATTATTAAGCTTTTATAGCATGAAATGTTAGGCTATATA 2160
Db 2101 CGCATTTTAAATGATCCGCTATTATTAAGCTTTTATAGCATGAAATGTTAGGCTATATA 2160
Qy 2161 ACATTGCGCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGCTTG 2220
Db 2161 ACATTGCGCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGCTTG 2220
Qy 2221 GAAGAGCCTGGACACTAACAAATCTACACCAAAATGCTCTTCAAAATACGTATGCACTGG 2280
Db 2221 GAAGAGCCTGGACACTAACAAATCTACACCAAAATGCTCTTCAAAATACGTATGCACTGG 2280
Qy 2281 ATAACTCTGAGAACACATCTAGTATTAACCTGAATAAGCAGAGCATCAAAATTAACAGACA 2340
Db 2281 ATAACTCTGAGAACACATCTAGTATTAACCTGAATAAGCAGAGCATCAAAATTAACAGACA 2340
Qy 2341 GAAACCGAAAGCTCTATATAAATGCTCAGAGTCTTTTATGATTTCTTTATGATTTCTTTATGGCATTCAA 2400
Db 2341 GAAACCGAAAGCTCTATATAAATGCTCAGAGTCTTTTATGATTTCTTTATGATTTCTTTATGGCATTCAA 2400
Qy 2401 CATATGTAATCAGAAAACAGGAAATTTTCAATTAATAATATGTTGTTGAAAT 2454
Db 2401 CATATGTAATCAGAAAACAGGAAATTTTCAATTAATAATATGTTGTTGAAAT 2454
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RESULT 12

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US-10-176-918-327
; Sequence 327, Application US/10176918
; Publication No. US200300275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC382
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 327
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-918-327
```

Query Match 100.08; Score 2454; DB 9; Length 2454;
Best Local Similarity 100.08; Pred. No. 0;

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Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGACTAATCTGTGGAGCAGTATTTATCCAGTATATCCAGGGTGCAGCCACACAGGACT 60
Db 1 GGACTAATCTGTGGAGCAGTATTTATCCAGTATATCCAGGGTGCAGCCACACAGGACT 60
Qy 61 GTGTGAAGGCTGTTTTTCTTTTAAATGTAATACCTCTCTCATCTCTTTCTTTTACAC 120
Db 61 GTGTGAAGGCTGTTTTTCTTTTAAATGTAATACCTCTCTCATCTCTTTCTTTTACAC 120
Qy 121 AGTGTCTGAGAACATTTTACATTTATAGATAAAGTAGTACATGTGGATACTTCTACTTTTA 180
Db 121 AGTGTCTGAGAACATTTTACATTTATAGATAAAGTAGTACATGTGGATACTTCTACTTTTA 180
Qy 181 GGAGSACTACTCTCTCTGACAGTCTTAGACTGCTTCTTCTACACTTAAGACACCATGAAG 240
Db 181 GGAGSACTACTCTCTCTGACAGTCTTAGACTGCTTCTTCTACACTTAAGACACCATGAAG 240
Qy 241 AGTATGTCTCTCTTATTTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCT 300
Db 241 AGTATGTCTCTCTTATTTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCT 300
Qy 301 ACATCGCACTGAAGAAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATG 360
Db 301 ACATCGCACTGAAGAAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATG 360
Qy 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Db 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Qy 421 GCCATTTTCTTCCATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 GCCATTTTCTTCCATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Qy 481 GAGTTGTACATGCTCAGATTTAGGTTTGCCTCAGTCCCAACCAACCAATTCATTTTGATA 540
Db 481 GAGTTGTACATGCTCAGATTTAGGTTTGCCTCAGTCCCAACCAACCAATTCATTTTGATA 540
Qy 541 CTGGAATGCTTGATCTTCAAAACAATAAAATTAAGGAAATCAAGAAATGATTTTAAAG 600
Db 541 CTGGAATGCTTGATCTTCAAAACAATAAAATTAAGGAAATCAAGAAATGATTTTAAAG 600
Qy 601 GACTCACTTCACTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 601 GACTCACTTCACTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Qy 661 AAGCCTTTCTAACCAACAAGAAAGTTCGGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 661 AAGCCTTTCTAACCAACAAGAAAGTTCGGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Qy 721 AAATACCACTTAATCTTCCCAATCATTTAGCAGAACTCAGAAATTCATGAAAATAAAGTTA 780
Db 721 AAATACCACTTAATCTTCCCAATCATTTAGCAGAACTCAGAAATTCATGAAAATAAAGTTA 780
Qy 781 AGAAAATACAAAGAGACACATTCAGAGGATGATGCTTTTACAGCTTTTGGAAATGAGTG 840
Db 781 AGAAAATACAAAGAGACACATTCAGAGGATGATGCTTTTACAGCTTTTGGAAATGAGTG 840
Qy 841 CAAACCTCTTGATAATAATGAGGATAGAGCCAGGGCATTTGAAGGGGTGACGGTGTTC 900
Db 841 CAAACCTCTTGATAATAATGAGGATAGAGCCAGGGCATTTGAAGGGGTGACGGTGTTC 900
Qy 901 ATATCAGAAATGCAGAAAGCAAACTGACCTCAGTCTTAAAGGCTTTACCACCACTTTAT 960
Db 901 ATATCAGAAATGCAGAAAGCAAACTGACCTCAGTCTTAAAGGCTTTACCACCACTTTAT 960
Qy 961 TGSAGCTTCACTTAGATTTATATAAATTTCAACAGTGGAACTTGAGGATTTTAAACGAT 1020
Db 961 TGSAGCTTCACTTAGATTTATATAAATTTCAACAGTGGAACTTGAGGATTTTAAACGAT 1020
Qy 1021 ACAGAGAACTACAAAGGCTGGGCTAGGAAACCAACAAATATCAGATATCGAAAATGGA 1080
Db 1021 ACAGAGAACTACAAAGGCTGGGCTAGGAAACCAACAAATATCAGATATCGAAAATGGA 1080
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1081 GTCTTCTTAACATACCACGCTGTGAGAGAAATACATTGGGAAACAATAAATAAAAAA 1140
Db GTCTTCTTAACATACCACGCTGTGAGAGAAATACATTGGGAAACAATAAATAAAAAA 1140
1141 TCCCTTCAGGATACCAGAGTTGAATACCTCCAGATATCTTCCCTTCATTCTTAATTCAA 1200
Db TCCCTTCAGGATACCAGAGTTGAATACCTCCAGATATCTTCCCTTCATTCTTAATTCAA 1200
1201 TTGCAAGAGTGGGAGTAAATGACTTCTGTCCAAACAGTGGCCAAAGATGAAGAAATCTTTAT 1260
Db TTGCAAGAGTGGGAGTAAATGACTTCTGTCCAAACAGTGGCCAAAGATGAAGAAATCTTTAT 1260
1261 ACAGTGCATAAGTTTATTCACAAACCCGCTGAAATCTCTGGAATGCAACCTGCAACAT 1320
Db ACAGTGCATAAGTTTATTCACAAACCCGCTGAAATCTCTGGAATGCAACCTGCAACAT 1320
1321 TTGCTTGTCTTTGACGAGAAATGCTGCTGAGCTTGGGAACTTTGGAATGTAATATTAG 1380
Db TTGCTTGTCTTTGACGAGAAATGCTGCTGAGCTTGGGAACTTTGGAATGTAATATTAG 1380
1381 TAATTGGTAAATGCCATTTAATAAGATTCAAAAATCCCTACATTTGGAATACTTTGAAC 1440
Db TAATTGGTAAATGCCATTTAATAAGATTCAAAAATCCCTACATTTGGAATACTTTGAAC 1440
1441 TCTATTAAATAGGTAGTATTATATACAAACCCGCTGAAATCTATCTCAAGTGGTAACTCC 1500
Db TCTATTAAATAGGTAGTATTATATACAAACCCGCTGAAATCTATCTCAAGTGGTAACTCC 1500
1501 ACTGACTTATTTATCACAGAAATTTCAACGGAATTTGCCAAACTATTGATACATAAG 1560
Db ACTGACTTATTTATCACAGAAATTTCAACGGAATTTGCCAAACTATTGATACATAAG 1560
1561 GGCTTGAGAGAAACAAGCATCTATTGCAGTTTCTCTTTTGGTACAAATGATCTTACATA 1620
Db GGCTTGAGAGAAACAAGCATCTATTGCAGTTTCTCTTTTGGTACAAATGATCTTACATA 1620
1621 AATCTCATGCTTGACCATTCCTTTCTTACATAAAGAAAGTAAAGTATTCGGTATTTAAC 1680
Db AATCTCATGCTTGACCATTCCTTTCTTACATAAAGAAAGTAAAGTATTCGGTATTTAAC 1680
1681 ACTTCTGATCAAGACACATTTTAAAGAACTGCTGTAATGGAATGCTTCACTAGC 1740
Db ACTTCTGATCAAGACACATTTTAAAGAACTGCTGTAATGGAATGCTTCACTAGC 1740
1741 AAAATTTGCTCTTTTCATTTGCTGTAGAAAAACAGAAATTAACAAGACAGTAATGTGA 1800
Db AAAATTTGCTCTTTTCATTTGCTGTAGAAAAACAGAAATTAACAAGACAGTAATGTGA 1800
1801 AGAGTGCATTACACTATCTTATCTTTAGTAACTTTGGGTAGTACTGTAATATTTTAAAT 1860
Db AGAGTGCATTACACTATCTTATCTTTAGTAACTTTGGGTAGTACTGTAATATTTTAAAT 1860
1861 CATCTTAAAGTATGATTGATATAATCTTATTTGAAATACCTTATCATGCTTGTAGAGCC 1920
Db CATCTTAAAGTATGATTGATATAATCTTATTTGAAATACCTTATCATGCTTGTAGAGCC 1920
1921 GTCTTTATGTTTAAACTAAATTTCTTAAATAAGCCTTCAGTAAATGTTTCATTACCAAC 1980
Db GTCTTTATGTTTAAACTAAATTTCTTAAATAAGCCTTCAGTAAATGTTTCATTACCAAC 1980
1981 TTGATAAATGCTACTCATAGAGCTGGTTGGGCTATAGCATATGCTTTTTTTTTTTTA 2040
Db TTGATAAATGCTACTCATAGAGCTGGTTGGGCTATAGCATATGCTTTTTTTTTTTTA 2040
2041 ATTATTACCTGATTTAAATCTCTCTAAACGCTGTAGTGGTTTCATAAAATCTGTAAT 2100
Db ATTATTACCTGATTTAAATCTCTCTAAACGCTGTAGTGGTTTCATAAAATCTGTAAT 2100
2101 CGCATTTTAAATGATCCGCTATTATAGCTTTTAAATAGCATGAAATTTGTTAGGCTATATA 2160
Db CGCATTTTAAATGATCCGCTATTATAGCTTTTAAATAGCATGAAATTTGTTAGGCTATATA 2160

2161 ACATTGCCACTTCAACTCTAAGGAATATTTTTCAGATATCCCTTTTGAAGACCTTGTGTTG 2220
Db ACATTGCCACTTCAACTCTAAGGAATATTTTTCAGATATCCCTTTTGAAGACCTTGTGTTG 2220
2221 GAAGAGCCTGGACACTAACAATTTCTACACCAAAATTTGCTCTTCAAAATACGCTATGGACTGG 2280
Db GAAGAGCCTGGACACTAACAATTTCTACACCAAAATTTGCTCTTCAAAATACGCTATGGACTGG 2280
2281 ATAACCTCTGAGAAACACATCTAGTATAAAGTGAATAAGCAGACATCAAAATTAACAGACA 2340
Db ATAACCTCTGAGAAACACATCTAGTATAAAGTGAATAAGCAGACATCAAAATTAACAGACA 2340
2341 GAAACCGAAGCTCTATATAAATGCTCAGAGTTCTTTATGATTTCTTATTTGGCATTCAA 2400
Db GAAACCGAAGCTCTATATAAATGCTCAGAGTTCTTTATGATTTCTTATTTGGCATTCAA 2400
2401 CATATGTAATAACAGAAACAGGAAATTTTTCATTAATAAATATTTGGTTTCAAAAT 2454
Db CATATGTAATAACAGAAACAGGAAATTTTTCATTAATAAATATTTGGTTTCAAAAT 2454

RESULT 13

US-10-176-921-327

Sequence 327, Application US/10176921

Publication No. US20030027276A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3330R1C288

CURRENT APPLICATION NUMBER: US/10/176, 921

CURRENT FILING DATE: 2002-06-20

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 327

LENGTH: 2454

TYPE: DNA

ORGANISM: Homo Sapien

US-10-176-921-327

Query Match 100.0%; Score 2454; DB 9; Length 2454;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACTAATCTGTGGAGCAGCTTTATTCAGTATCACCCAGGGTGCAGCCACACAGGACT 60

Db 1 GGACTAATCTGTGGAGCAGCTTTATTCAGTATCACCCAGGGTGCAGCCACACAGGACT 60

QY 61 GTGTTGAAGGGTGTGTTTTTCTTTTAAATGTAATACCTCTCTATCTTTCTTCTTACAC 120

Db 61 GTGTTGAAGGGTGTGTTTTTCTTTTAAATGTAATACCTCTCTATCTTTCTTCTTACAC 120

QY 121 AGTGTCTGAGAACATTTACATTTAGATAAGTAGTACATGTTGATAACTTCTACTTTTA 180

Db 121 AGTGTCTGAGAACATTTACATTTAGATAAGTAGTACATGTTGATAACTTCTACTTTTA 180

QY 181 GGAGGACTACTCTCTTCTTGACAGTCTAGAGTGGTCTTCTTACATTAAGACACCATGAAG 240

Db	181	GGAGGACTACTCTCTCTGACAGTCCTAGACTGGTCTTCTACACTAAGACACCATGAAGG	240
Qy	241	AGATATGCTCCTATTAATTCCTGGCTTGTGCTCTGCCAAACCCCTCTCTTAGCCCTTCAC	300
Db	241	AGTATGCTCCTATTAATTCCTGGCTTGTGCTCTGCCAAACCCCTCTCTTAGCCCTTCAC	300
Qy	301	ACATCGCACTGAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATG	360
Db	301	ACATCGCACTGAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATG	360
Qy	361	ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	420
Db	361	ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	420
Qy	421	GCCATTTTTTCCATTTGATCTGTTTCCAAATGTGTCCTATTTGGATGTCAGTGTATTCAC	480
Db	421	GCCATTTTTTCCATTTGATCTGTTTCCAAATGTGTCCTATTTGGATGTCAGTGTATTCAC	480
Qy	481	GAGTTGTACATTTGCTCAGATTTTAGTTTGTACCTCAGTCCCAACCAATTTTAAAG	540
Db	481	GAGTTGTACATTTGCTCAGATTTTAGTTTGTACCTCAGTCCCAACCAATTTTAAAG	540
Qy	541	CTCGAATGCTTGATCTTCAAAACAATAAATTAAGGAAATCAAGAAATGATTTTAAAG	600
Db	541	CTCGAATGCTTGATCTTCAAAACAATAAATTAAGGAAATCAAGAAATGATTTTAAAG	600
Qy	601	GACTCACTTCACCTTATGCTGTCATCTGATCCTGAACAAACAAGCTTAACGAAGATTCACCCAA	660
Db	601	GACTCACTTCACCTTATGCTGTCATCTGATCCTGAACAAACAAGCTTAACGAAGATTCACCCAA	660
Qy	661	AAGCCTTTCTAACCCACAAAGAAGTTGCGAAGGCTGTATCTGTCCCAAACTCAACTAAGTG	720
Db	661	AAGCCTTTCTAACCCACAAAGAAGTTGCGAAGGCTGTATCTGTCCCAAACTCAACTAAGTG	720
Qy	721	AAATPACCACTTAATCTTCCCAATCAATTAGCGAAGCTCAGAAATTCATGAAATTAAGTTA	780
Db	721	AAATPACCACTTAATCTTCCCAATCAATTAGCGAAGCTCAGAAATTCATGAAATTAAGTTA	780
Qy	781	AGAAATFACAAAAGGACACATTCAAAGGAATGAATGCTTTACAGTTTTCGAAATGAGTG	840
Db	781	AGAAATFACAAAAGGACACATTCAAAGGAATGAATGCTTTACAGTTTTCGAAATGAGTG	840
Qy	841	CAAAACCTCTTGATAAATGGGATAGAGCCAGGGCATTTGAAGGGGTGACGGTGTTC	900
Db	841	CAAAACCTCTTGATAAATGGGATAGAGCCAGGGCATTTGAAGGGGTGACGGTGTTC	900
Qy	901	ATATCAGAAATGAGAGCAAACTGACCTCAGTTTCTTAAAGGTTACACCAACTTTAT	960
Db	901	ATATCAGAAATGAGAGCAAACTGACCTCAGTTTCTTAAAGGTTACACCAACTTTAT	960
Qy	961	TGGAGCTTCACTTAGATTATTAATAAAATTTCAACAGTGAACCTTGAGGATTTTAAACGAT	1020
Db	961	TGGAGCTTCACTTAGATTATTAATAAAATTTCAACAGTGAACCTTGAGGATTTTAAACGAT	1020
Qy	1021	ACAAAGAACTACAAAGGCTGGGCTTAGGAAACAAACAAATACAGATATTCGAAATGGGA	1080
Db	1021	ACAAAGAACTACAAAGGCTGGGCTTAGGAAACAAACAAATACAGATATTCGAAATGGGA	1080
Qy	1081	GTCTTGCTTAACATACACAGTGTGAGAGAAATACATTTGGAAACAAATAAACTTAAAAAAA	1140
Db	1081	GTCTTGCTTAACATACACAGTGTGAGAGAAATACATTTGGAAACAAATAAACTTAAAAAAA	1140
Qy	1141	TCCTCTCAGATTTACAGAGCTTGAATACCTCCAGATATCTTCCCTTCATCTTAATTCAA	1200
Db	1141	TCCTCTCAGATTTACAGAGCTTGAATACCTCCAGATATCTTCCCTTCATCTTAATTCAA	1200
Qy	1201	TTGCAAGAGTGGGATTAATGACTTCTGTCCAAAGTCCCAAGAGTGAAGAAATCTTTAT	1260
Db	1201	TTGCAAGAGTGGGATTAATGACTTCTGTCCAAAGTCCCAAGAGTGAAGAAATCTTTAT	1260
Qy	1261	ACAGTGCAATTAAGTTTATTCACAAACCCGGTGAATTAACCTGGGAAATGCAACCTGCAACAT	1320
Db	1261	ACAGTGCAATTAAGTTTATTCACAAACCCGGTGAATTAACCTGGGAAATGCAACCTGCAACAT	1320

Dd	1361	ACAGTGCAAATAAGTTTTATTCAACAACCCTGGTGGAATACTGGGAAATTCGCAACCTGCAACAT	1320
Qy	1321	TTCGTTGTGTTTTGAGCAGAATAGTGTTCCAGCTTGGGAACCTTTGGAATCTAATAATTAG	1380
Dd	1321	TTCGTTGTGTTTTGAGCAGAATAGTGTTCCAGCTTGGGAACCTTTGGAATCTAATAATTAG	1380
Qy	1381	TAATTTGGTAATGTCCTATTTAATAAAGATTCAAANAATCCCACATTTGGGAATACTTTGAAC	1440
Dd	1381	TAATTTGGTAATGTCCTATTTAATAAAGATTCAAANAATCCCACATTTGGGAATACTTTGAAC	1440
Qy	1441	TCTATTAATAATGCTAGTATATATATACAAAGCAAAATATCTATTTCTCAAGTGGTAAGTCC	1500
Dd	1441	TCTATTAATAATGCTAGTATATATATACAAAGCAAAATATCTATTTCTCAAGTGGTAAGTCC	1500
Qy	1501	ACTGACATATTTATGACAAAGAAATTTCAACGGAAATTTGCCAAAATCTATTGATACATAAG	1560
Dd	1501	ACTGACATATTTATGACAAAGAAATTTCAACGGAAATTTGCCAAAATCTATTGATACATAAG	1560
Qy	1561	GGGTTGAGAGAAACAAGCATCTATTGCAGTTTCCTTTTGGCGTACAAAATGATCTTACATA	1620
Dd	1561	GGGTTGAGAGAAACAAGCATCTATTGCAGTTTCCTTTTGGCGTACAAAATGATCTTACATA	1620
Qy	1621	AATCTCATGCTTGACCATTCCTTCTTTCATACAAAAAGTAGAGATTCCGGTATTTAAC	1680
Dd	1621	AATCTCATGCTTGACCATTCCTTCTTTCATACAAAAAGTAGAGATTCCGGTATTTAAC	1680
Qy	1681	ACTTTGTTATCAAGCACATTTTAAAAAGAACTGTACTGTAATGGAATGCTTGACATTAGC	1740
Dd	1681	ACTTTGTTATCAAGCACATTTTAAAAAGAACTGTACTGTAATGGAATGCTTGACATTAGC	1740
Qy	1741	AAAAATTTGTCCTTTTCATTTCGTTGTAGAAAAACAGAAATTAACAAAGCAGTAATGTGA	1800
Dd	1741	AAAAATTTGTCCTTTTCATTTCGTTGTAGAAAAACAGAAATTAACAAAGCAGTAATGTGA	1800
Qy	1801	AGAGTGCAATACACATNTCTTATCTTTAGTAACCTTGGGTAGTACTGTAATATTTTAAAT	1860
Dd	1801	AGAGTGCAATACACATNTCTTATCTTTAGTAACCTTGGGTAGTACTGTAATATTTTAAAT	1860
Qy	1861	CATCTTAAAGTATCATTTTGATATAAATCTTATGAAATTACCTTATCATGTCCTTAGAGCCC	1920
Dd	1861	CATCTTAAAGTATCATTTTGATATAAATCTTATGAAATTACCTTATCATGTCCTTAGAGCCC	1920
Qy	1921	GTCCTTATGTTTAAACATAATTTCTTAAAAATAAGCCTTCAGTAAATGTTTCATTACCAAC	1980
Dd	1921	GTCCTTATGTTTAAACATAATTTCTTAAAAATAAGCCTTCAGTAAATGTTTCATTACCAAC	1980
Qy	1981	TTGATAAATGCTACTCATAGAGCTGGTTTGGGCTATAGCATATGCTTTTTTTTTTTTA	2040
Dd	1981	TTGATAAATGCTACTCATAGAGCTGGTTTGGGCTATAGCATATGCTTTTTTTTTTTTA	2040
Qy	2041	ATTTATACCTGATTTAAAAATCTCTGTFAAAACGTTAGTGTTCATATAAACTGTAAC	2100
Dd	2041	ATTTATACCTGATTTAAAAATCTCTGTFAAAACGTTAGTGTTCATATAAACTGTAAC	2100
Qy	2101	CGCATTTTAAATGATCGCTATTTAAGCTTTTAAAGCATGAAAAATGTTAGGCTATATA	2160
Dd	2101	CGCATTTTAAATGATCGCTATTTAAGCTTTTAAAGCATGAAAAATGTTAGGCTATATA	2160
Qy	2161	ACATITGCCACTTCAACTCTAAGGAATATTTTTCAGATATCCCTTGGAGACGCTTCTTG	2220
Dd	2161	ACATITGCCACTTCAACTCTAAGGAATATTTTTCAGATATCCCTTGGAGACGCTTCTTG	2220
Qy	2221	GAAGAGCTTGACACTAACAAATCTCACCAAAATTCCTCTCAAAATAGCTATGGACTGG	2280
Dd	2221	GAAGAGCTTGACACTAACAAATCTCACCAAAATTCCTCTCAAAATAGCTATGGACTGG	2280
Qy	2281	ATAACTCTGAGAAACACATCTAGTATAACTGTAATAAGCAGAGCATCAAAATTAACAGACA	2340
Dd	2281	ATAACTCTGAGAAACACATCTAGTATAACTGTAATAAGCAGAGCATCAAAATTAACAGACA	2340
Qy	2341	GAACCCGAAAGCTCTATATAAAATGCTCAGAGTTCTTTTATGTATTTCTTAAATGGCAATCAA	2400
Dd	2341	GAACCCGAAAGCTCTATATAAAATGCTCAGAGTTCTTTTATGTATTTCTTAAATGGCAATCAA	2400

Qy 2401 CATATGTAATAATCAGAAACAGGAAATTTTCATTAATAAATATATGGTTTGAAT 2454
Db CATATGTAATAATCAGAAACAGGAAATTTTCATTAATAAATATATGGTTTGAAT 2454

RESULT 14

US-10-137-865-327
: Sequence 327, Application US/10137865
: Publication No. US20030032155A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Geritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3330R1C154
: CURRENT APPLICATION NUMBER: US/10/137.865
: CURRENT FILING DATE: 2002-05-03
: Prior Application removed - See Palm or File Wrapper
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 327
: LENGTH: 2454
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-137-865-327

Query Match 100.08; Score 2454; DB 9; Length 2454;
Best Local Similarity 100.08; Pred. No. 0;
Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GGACTAATCTCTGGGAGCAGTTTATCCAGTATCACCCAGGGTGCAGCCACACACAGGACT 60
1 GGACTAATCTCTGGGAGCAGTTTATCCAGTATCACCCAGGGTGCAGCCACACACAGGACT 60
61 GTGTGAGGGGTGTTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTCTTACAC 120
61 GTGTGAGGGGTGTTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTCTTACAC 120
121 AGTGTCTGAGAACATTTACATATATAGATAGTACATGTTGTAATACCTTCTTCTTCTT 180
121 AGTGTCTGAGAACATTTACATATATAGATAGTACATGTTGTAATACCTTCTTCTTCTT 180
181 GGAGGACTACTCTCTCTGACAGCTCTAGCTGTTCTTCTACACTAAGACACCATGAAGG 240
181 GGAGGACTACTCTCTCTGACAGCTCTAGCTGTTCTTCTACACTAAGACACCATGAAGG 240
241 AGTATGCTCCTCTATTTATTTCTGGCTTTGCTCTGCGAAACCCCTCTTTTAGCCCTTAC 300
241 AGTATGCTCCTCTATTTATTTCTGGCTTTGCTCTGCGAAACCCCTCTTTTAGCCCTTAC 300
301 ACATCGCACTGAAGAATATGATGCTGAAGGATATGGAAGACACACAGATGATGATGATG 360
301 ACATCGCACTGAAGAATATGATGCTGAAGGATATGGAAGACACACAGATGATGATGATG 360
361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420

Qy 421 GCCATTTTTCATTTGATCTGTTTCCATGTCCTCATTTGGATGTCAGTCTATTTCAC 480
Db 421 GCCATTTTTCATTTGATCTGTTTCCATGTCCTCATTTGGATGTCAGTCTATTTCAC 480
Qy 481 GAGTTGTACATTTGCTCAGATTTAGTTTGTAGTCTCAGTCCCAACCAACATTCCTCATTTGATA 540
Db 481 GAGTTGTACATTTGCTCAGATTTAGTTTGTAGTCTCAGTCCCAACCAACATTCCTCATTTGATA 540
Qy 541 CTCGAATGCTTTGATCTTTCAAAACAATAAATAAGGAAATCAAAAGAAATGATTTTAAAG 600
Db 541 CTCGAATGCTTTGATCTTTCAAAACAATAAATAAGGAAATCAAAAGAAATGATTTTAAAG 600
Qy 601 GACTCACTTTCATTTATGTTGCTGATCTGACACACACACACAGCTAACGAAGATTCACCCAA 660
Db 601 GACTCACTTTCATTTATGTTGCTGATCTGACACACACACACAGCTAACGAAGATTCACCCAA 660
Qy 661 AAGCTTTTCTAAACCACAAAGAGTTTGGAGGGTGTATCTGTCCCAACAATACTAAAGTG 720
Db 661 AAGCTTTTCTAAACCACAAAGAGTTTGGAGGGTGTATCTGTCCCAACAATACTAAAGTG 720
Qy 721 AAATACCACATTAATCTTCCCAAAATCATTAGCAGAACTCAGAAATTCATGAAATAAAGTTA 780
Db 721 AAATACCACATTAATCTTCCCAAAATCATTAGCAGAACTCAGAAATTCATGAAATAAAGTTA 780
Qy 781 AGAAATACAAAGACACATTTCAAAGGAATGAATGCTTTTACACGTTTGGAAATGAGTG 840
Db 781 AGAAATACAAAGACACATTTCAAAGGAATGAATGCTTTTACACGTTTGGAAATGAGTG 840
Qy 841 CAAACCTCTTTGATAAATAGGATAGAGCCAGGGCATTTGAAGGGTGCAGGTGTTCC 900
Db 841 CAAACCTCTTTGATAAATAGGATAGAGCCAGGGCATTTGAAGGGTGCAGGTGTTCC 900
Qy 901 ATATCAGAAATTCGAGAAACAACTGACCTCAGTTCCTTAAAGGCTTACCACTTAT 960
Db 901 ATATCAGAAATTCGAGAAACAACTGACCTCAGTTCCTTAAAGGCTTACCACTTAT 960
Qy 961 TGGAGCTTCACTTAGATATATAAATTTCAACAGTGGAACTTCAGGATTTTAAACGAT 1020
Db 961 TGGAGCTTCACTTAGATATATAAATTTCAACAGTGGAACTTCAGGATTTTAAACGAT 1020
Qy 1021 ACAAGAACTACAAAGGCTGGCCCTAGGAAACAACAAATCACAGATATCGAAATGGGA 1080
Db 1021 ACAAGAACTACAAAGGCTGGCCCTAGGAAACAACAAATCACAGATATCGAAATGGGA 1080
Qy 1081 GTCTTGCTAACATACCACGCTGTGAGAGAAATACATTTGGAAACAATAAATCAAAAAA 1140
Db 1081 GTCTTGCTAACATACCACGCTGTGAGAGAAATACATTTGGAAACAATAAATCAAAAAA 1140
Qy 1141 TCCCTTCAGGATTTACCAGAGTTGAAATACCTCCAGATAATCTTCTTCATTTCAATCAA 1200
Db 1141 TCCCTTCAGGATTTACCAGAGTTGAAATACCTCCAGATAATCTTCTTCATTTCAATCAA 1200
Qy 1201 TTGCAAGAGTGGAGTAAATGACCTTCTCCAAAGTCCCAAGATGAAGAAATCTTTAT 1260
Db 1201 TTGCAAGAGTGGAGTAAATGACCTTCTCCAAAGTCCCAAGATGAAGAAATCTTTAT 1260
Qy 1261 ACAGTGAATAAGTTTATTTCAACAAACCCGGTGAATACTGGGAAATGCAACCTGCAACAT 1320
Db 1261 ACAGTGAATAAGTTTATTTCAACAAACCCGGTGAATACTGGGAAATGCAACCTGCAACAT 1320
Qy 1321 TTCGTTGTTTGGAGCAGATGAGTGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1380
Db 1321 TTCGTTGTTTGGAGCAGATGAGTGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1380
Qy 1381 TAATTTGTAATGTCCTATTAATAAGATTCAAAATCCCTACATTTTGGAAATGTAATAAG 1440
Db 1381 TAATTTGTAATGTCCTATTAATAAGATTCAAAATCCCTACATTTTGGAAATGTAATAAG 1440
Qy 1441 TCTATTAATAAGTGTAGTATATATATACAGCAAAATATCTTCTCAAGTGGTGAAGTCC 1500
Db 1441 TCTATTAATAAGTGTAGTATATATATATACAGCAAAATATCTTCTCAAGTGGTGAAGTCC 1500
Qy 1501 ACTGACTTATTTTATGACAAGAAATTTCAACGGAAATTTTCCAAACTATTTGATACATAAG 1560

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Db 1501 ACTGACTTATTTATGACAGAAATTTCAACGGAATTTTGCCAACTATTGTACATAAG 1560
QY 1561 GGGTTGAGAGAAACAAGCATCTATTGCGAGTTTCCTTTTTCGGGTACAAATGATCTTACATA 1620
Db 1561 GGGTTGAGAGAAACAAGCATCTATTGCGAGTTTCCTTTTTCGGGTACAAATGATCTTACATA 1620
QY 1621 AATCTCATGCTTGACCATCTCTTCTTCATACAAACAGAAATTAACAAAGACAGTAATTTAAAT 1680
Db 1621 AATCTCATGCTTGACCATCTCTTCTTCATACAAACAGAAATTAACAAAGACAGTAATTTAAAT 1680
QY 1681 ACTTCTTATCAGACACATTTAAAGAAAGACTGCTACTGTAATGGAATGCTTGACATTAGC 1740
Db 1681 ACTTCTTATCAGACACATTTAAAGAAAGACTGCTACTGTAATGGAATGCTTGACATTAGC 1740
QY 1741 AAAATTTGGCTCTTTCATTTGCTGTAGAAAACAGAAATTAACAAAGACAGTAATTTAAAT 1800
Db 1741 AAAATTTGGCTCTTTCATTTGCTGTAGAAAACAGAAATTAACAAAGACAGTAATTTAAAT 1800
QY 1801 AGAGTGCATACACTATCTTATCTTTAGTAACCTTGGGTAGTACGTAAATTTTAAAT 1860
Db 1801 AGAGTGCATACACTATCTTATCTTTAGTAACCTTGGGTAGTACGTAAATTTTAAAT 1860
QY 1861 CATCTTAAAGTATGATTTGATATAATCTTATGAAATTTACCTTATCATCTCTTAGAGCCC 1920
Db 1861 CATCTTAAAGTATGATTTGATATAATCTTATGAAATTTACCTTATCATCTCTTAGAGCCC 1920
QY 1921 GTCTTTATGTTTAAACTAATTTCTTAAATAAGCCTTCAGTAAATGTTTCATTACCAAC 1980
Db 1921 GTCTTTATGTTTAAACTAATTTCTTAAATAAGCCTTCAGTAAATGTTTCATTACCAAC 1980
QY 1981 TTGATAAATGCTACTCATAGAGCTGGTTGGGGCTATAGCATATGCTTTTTTTTTTTA 2040
Db 1981 TTGATAAATGCTACTCATAGAGCTGGTTGGGGCTATAGCATATGCTTTTTTTTTTTA 2040
QY 2041 ATTATTAACCTGATTTAAATCTCTGTAAGAGCTGCTAGTGTTCATAAATCTGTAAC 2100
Db 2041 ATTATTAACCTGATTTAAATCTCTGTAAGAGCTGCTAGTGTTCATAAATCTGTAAC 2100
QY 2101 CGCATTTAATGATCGCTATTATTAAGCTTTTAAAGCATGAAATTTGTTAGGCTATATA 2160
Db 2101 CGCATTTAATGATCGCTATTATTAAGCTTTTAAAGCATGAAATTTGTTAGGCTATATA 2160
QY 2161 ACATGCGCACTTCAACTCTAAGGAATATTTTTCAGATATCCCTTTGGAAGACCTGCTTG 2220
Db 2161 ACATGCGCACTTCAACTCTAAGGAATATTTTTCAGATATCCCTTTGGAAGACCTGCTTG 2220
QY 2221 GAAGAGCCTGGACACTAACAAATTTCTACACAAATTTCTCTCAAAATGCTATGGAGCTG 2280
Db 2221 GAAGAGCCTGGACACTAACAAATTTCTACACAAATTTCTCTCAAAATGCTATGGAGCTG 2280
QY 2281 ATAACTCTGAGAAACACATCTAGTATACTGAATAAGCAGAGCATCAAAATTAACAGACA 2340
Db 2281 ATAACTCTGAGAAACACATCTAGTATACTGAATAAGCAGAGCATCAAAATTAACAGACA 2340
QY 2341 GAAACCGAAGCTCTATATAAATGCTCAGAGTTCTTTATGATATTTCTTATGCGATTCAA 2400
Db 2341 GAAACCGAAGCTCTATATAAATGCTCAGAGTTCTTTATGATATTTCTTATGCGATTCAA 2400
QY 2401 CATATCTAAATCAGAAACAGGAAATTTTCATTAATAATATGCTTTGAAAT 2454
Db 2401 CATATCTAAATCAGAAACAGGAAATTTTCATTAATAATATGCTTTGAAAT 2454
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RESULT 15

US-10-140-474-327

; Sequence 327, Application US/10140474

; Publication No. US20030032156A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DePorge, Laura

; APPLICANT: Desnoyers, Luc

```
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C162
; CURRENT APPLICATION NUMBER: US/10/140,474
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 327
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-140-474-327
```

Query Match 100.0%; Score 2454; DB 9; Length 2454;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGACTAATCTGTGGGAGCAGTATTTCCAGTAGTATCACCAGGGTGCAGCCACACAGGACT 60
Db 1 GGACTAATCTGTGGGAGCAGTATTTCCAGTAGTATCACCAGGGTGCAGCCACACAGGACT 60
QY 61 GTGTGAAGGGTGTCTTTTCTTTTAAATGTAATACCTCTCATCTTTCTTCTTACAC 120
Db 61 GTGTGAAGGGTGTCTTTTCTTTTAAATGTAATACCTCTCATCTTTCTTCTTACAC 120
QY 121 AGTGCTGAGAACATTTACATTATAGATAAGTAGTAGTACATGGTGGATAAATCTTCTACTTTTA 180
Db 121 AGTGCTGAGAACATTTACATTATAGATAAGTAGTAGTACATGGTGGATAAATCTTCTACTTTTA 180
QY 181 GGAGGACTACTCTCTCTGACAGTCTTAGACTGGTCTTCTACACTAAGACACATGAAG 240
Db 181 GGAGGACTACTCTCTCTGACAGTCTTAGACTGGTCTTCTACACTAAGACACATGAAG 240
QY 241 AGTATGTGCTCTATTTATTCCTGGCTTTGCTGCTGCCAAACCTCTTTTAGCCCTTCAC 300
Db 241 AGTATGTGCTCTATTTATTCCTGGCTTTGCTGCTGCCAAACCTCTTTTAGCCCTTCAC 300
QY 301 ACATCGCACTGAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATG 360
Db 301 ACATCGCACTGAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATG 360
QY 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Db 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 421 GCCATTTTTCCTATTTGATCTGTTTCCAAATGTGCTCAATTTGGATGCTAGTCTATTTCAC 480
Db 421 GCCATTTTTCCTATTTGATCTGTTTCCAAATGTGCTCAATTTGGATGCTAGTCTATTTCAC 480
QY 481 GAGTTGTACATTTGCTCAGATTTTAGGTTTTCACCTCAGTCCCAACCAACATTTCCATTGATA 540
Db 481 GAGTTGTACATTTGCTCAGATTTTAGGTTTTCACCTCAGTCCCAACCAACATTTCCATTGATA 540
QY 541 CTCGAATGCTTGTATCTTCAAAACATAAATAAAGAAATTAAGAAATTAAGAAATTAAG 600
Db 541 CTCGAATGCTTGTATCTTCAAAACATAAATAAAGAAATTAAGAAATTAAGAAATTAAG 600
QY 601 GACTCATTCTACTTTATGCTCTGATCCTCAACAAACACAGCTAACGAAGATTTCACCCAA 660
Db 601 GACTCATTCTACTTTATGCTCTGATCCTCAACAAACACAGCTAACGAAGATTTCACCCAA 660
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QY 661 AAGCTTTTCTAACCCACAAGAGTTGCGAAGCTCTATCTGTCCACACATCAACTAAGTG 720
Db 661 AAGCTTTTCTAACCCACAAGAGTTGCGAAGCTCTATCTGTCCACACATCAACTAAGTG 720
QY 721 AAATACCACTTAATCTCCCAATCATTTAGCAGAACTCAGAAATTCATGAAATAAAGTTA 780
Db 721 AAATACCACTTAATCTCCCAATCATTTAGCAGAACTCAGAAATTCATGAAATAAAGTTA 780
QY 781 AGAAATACAAAGGACACATTCAAAGGAATGAATGCTTTACACGCTTTTGGAAATGAGTG 840
Db 781 AGAAATACAAAGGACACATTCAAAGGAATGAATGCTTTACACGCTTTTGGAAATGAGTG 840
QY 841 CAACCCCTCTTGATATAATGGGATAGAGCCAGGGGCATTTGAAGGGGTGACGGTGTCC 900
Db 841 CAACCCCTCTTGATATAATGGGATAGAGCCAGGGGCATTTGAAGGGGTGACGGTGTCC 900
QY 901 ATATCAGAAATTCGAGAACCAAACTGACCTCAGTTCCTTAAAGGCTTACACCAACTTTAT 960
Db 901 ATATCAGAAATTCGAGAACCAAACTGACCTCAGTTCCTTAAAGGCTTACACCAACTTTAT 960
QY 961 TGGAGCTTCACCTAGATTAATAAATTTCAACAGTGGAACTTGAAGGGGTGACGGTGTCC 1020
Db 961 TGGAGCTTCACCTAGATTAATAAATTTCAACAGTGGAACTTGAAGGGGTGACGGTGTCC 1020
QY 1021 ACAAGAACTCAAAAGGCTGGCCCTAGGAAACAACAATAACAGATATCGAAATGGGA 1080
Db 1021 ACAAGAACTCAAAAGGCTGGCCCTAGGAAACAACAATAACAGATATCGAAATGGGA 1080
QY 1081 GTCTTGCTTAACATACACGCTGTGAGAGAAATACATTTGGAAACAATAAATCAAAAAA 1140
Db 1081 GTCTTGCTTAACATACACGCTGTGAGAGAAATACATTTGGAAACAATAAATCAAAAAA 1140
QY 1141 TCCCTTCAGGATACCAAGTGGAAATACCTCCAGATTAATCTTCCTTCATTTCAATTCAA 1200
Db 1141 TCCCTTCAGGATACCAAGTGGAAATACCTCCAGATTAATCTTCCTTCATTTCAATTCAA 1200
QY 1201 TTGCAAGAGTGGAGTAATGACTCTGTCCAAAGTGGCCAAAGATGAGAAATCTTTAT 1260
Db 1201 TTGCAAGAGTGGAGTAATGACTCTGTCCAAAGTGGCCAAAGATGAGAAATCTTTAT 1260
QY 1261 ACAGTGCAATTAAGTTTATCAACACCCGGTGAAATCTGGAAATGCAACCTGCAACAT 1320
Db 1261 ACAGTGCAATTAAGTTTATCAACACCCGGTGAAATCTGGAAATGCAACCTGCAACAT 1320
QY 1321 TTCGTTGTTTGTGAGCAGAAATGAGTGTTCAGCTTGGGAATTTTGGAAATGATTAATAG 1380
Db 1321 TTCGTTGTTTGTGAGCAGAAATGAGTGTTCAGCTTGGGAATTTTGGAAATGATTAATAG 1380
QY 1381 TAATTTGTTAATGTCATTAATAAAGATTCAAAATCCCTACATTTGGAATCTTGAAC 1440
Db 1381 TAATTTGTTAATGTCATTAATAAAGATTCAAAATCCCTACATTTGGAATCTTGAAC 1440
QY 1441 TCTATTAATAATGTTAGTATTATATATCAAGCAATATCTATCTCAAGTGGTAAAGTCC 1500
Db 1441 TCTATTAATAATGTTAGTATTATATATCAAGCAATATCTATCTCAAGTGGTAAAGTCC 1500
QY 1501 ACTGACTTATTTATGACAAGAAATTTTCAACGGAAATTTTGGCAAACTATTGATACATAAG 1560
Db 1501 ACTGACTTATTTATGACAAGAAATTTTCAACGGAAATTTTGGCAAACTATTGATACATAAG 1560
QY 1561 GGGTTGAGAGAAACAGCATCTATTGCGAGTTTCCCTTTTGGGTACAAATGATCTTACATA 1620
Db 1561 GGGTTGAGAGAAACAGCATCTATTGCGAGTTTCCCTTTTGGGTACAAATGATCTTACATA 1620
QY 1621 AATCTCATGCTTGACCATCTCTCTTCATACAAAAGTAAAGATATTCGGTATTTAAC 1680
Db 1621 AATCTCATGCTTGACCATCTCTCTTCATACAAAAGTAAAGATATTCGGTATTTAAC 1680
QY 1681 ACTTTGTTTATCAAGCACATTTTAAAGAACTGTAAGTAAATGGAATGCTTGACTTAGC 1740
Db 1681 ACTTTGTTTATCAAGCACATTTTAAAGAACTGTAAGTAAATGGAATGCTTGACTTAGC 1740

QY 1741 AAAATTTGTGCTCTTTTCATTTTGTCTGTAGAAAAAGAAATTAACAAAGACAGTAAATGTA 1800
Db 1741 AAAATTTGTGCTCTTTTCATTTTGTCTGTAGAAAAAGAAATTAACAAAGACAGTAAATGTA 1800
QY 1801 AGAGTGCAATTAACATTAATCTTTTATTTAGTAACCTTTGGTAGTACTGTAATATTTTAAAT 1860
Db 1801 AGAGTGCAATTAACATTAATCTTTTATTTAGTAACCTTTGGTAGTACTGTAATATTTTAAAT 1860
QY 1861 CATCTTAAAGTATGATTTGATATAATCTTTTAAATTAACCTTTATCATGCTTTAGAGCCC 1920
Db 1861 CATCTTAAAGTATGATTTGATATAATCTTTTAAATTAACCTTTATCATGCTTTAGAGCCC 1920
QY 1921 GTCTTTATGCTTTTAAACCTAAATTTCTTAAATAAAGCCTTCAGTAAATGCTTCATTACCAAC 1980
Db 1921 GTCTTTATGCTTTTAAACCTAAATTTCTTAAATAAAGCCTTCAGTAAATGCTTCATTACCAAC 1980
QY 1981 TTGATAAATGCTTACTCATAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTA 2040
Db 1981 TTGATAAATGCTTACTCATAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTA 2040
QY 2041 ATTATTACCTGATTTTAAATACTCTGTAAAAACGCTGTAGTCTTTCATATAAATCTGTAAC 2100
Db 2041 ATTATTACCTGATTTTAAATACTCTGTAAAAACGCTGTAGTCTTTCATATAAATCTGTAAC 2100
QY 2101 CGCATTTTAAATGATCCGCTTATTATAAGCTTTTAAATAGCATGAAATTTGAGGCTATATA 2160
Db 2101 CGCATTTTAAATGATCCGCTTATTATAAGCTTTTAAATAGCATGAAATTTGAGGCTATATA 2160
QY 2161 ACATTGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTTGCTTG 2220
Db 2161 ACATTGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTTGCTTG 2220
QY 2221 GAAGAGCTTGGACACTTAACAATTTACACCAAAATTTGCTCTTCAAAATAGGTATGACTGG 2280
Db 2221 GAAGAGCTTGGACACTTAACAATTTACACCAAAATTTGCTCTTCAAAATAGGTATGACTGG 2280
QY 2281 ATAACTCTCAGAAAAACACATCTAGTATACTGAATAAGCAGAGCATCAAAATTAACAGACA 2340
Db 2281 ATAACTCTCAGAAAAACACATCTAGTATACTGAATAAGCAGAGCATCAAAATTAACAGACA 2340
QY 2341 GAAACCGAAAGCTCTATATAAATGCTTCAGAGTTCTTTTATGATTTCTTATTTGGCAATCAA 2400
Db 2341 GAAACCGAAAGCTCTATATAAATGCTTCAGAGTTCTTTTATGATTTCTTATTTGGCAATCAA 2400
QY 2401 CATATGTAATAATCAGAAAAACAGGGAAATTTTCATTAAAAAATTTGGTTGAAAT 2454
Db 2401 CATATGTAATAATCAGAAAAACAGGGAAATTTTCATTAAAAAATTTGGTTGAAAT 2454

Search completed: May 31, 2003, 13:43:57
Job time : 347 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 31, 2003, 12:40:22 ; Search time 306 Seconds
(without alignments)
2789.240 Million cell updates/sec

Title: US-09-944-884-2

Perfect score: 1932
Sequence: 1 MKEYVLLFLALCAKPPFS.....PATFRCVLSRMSVQLNGFM 379

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=N_Geneseq_101002 -OPWR=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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22: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1992	100.0	2454	20	Human PRO241 nucle
2	1992	100.0	2454	22	Human CDNA sequenc
3	1992	100.0	2454	24	Human angiogenesis
4	1992	100.0	2454	24	Human PRO241 CDNA
5	1992	100.0	2454	21	Human PRO241 CDNA
6	1968	98.8	1548	22	Human polynucleoti
7	1828	91.8	1492	23	DNA encoding novel
8	1799	90.3	2305	22	Mouse bone/cartila
9	1799	90.3	2305	24	Murine CDNA isolat
10	1517	76.2	2089	22	Human CDNA sequenc
11	1293	64.9	896	22	Human neuroblastom
12	1235	61.5	854	22	Human CDNA clone (
13	1040.5	52.2	2446	16	Rat biglycan CDNA.
14	1034	51.9	1685	22	Human DNA encoding
15	1034	51.9	1685	22	Human biglycan enc
16	1034	51.9	1685	24	Breast cancer rela
17	1034	51.9	1685	24	Breast cancer rela
18	1034	51.9	1685	24	Stomach cancer rel
19	1034	51.9	2296	24	Human CDNA encodin
20	1034	51.9	2367	20	Human prostate tum
21	1034	51.9	2384	20	Human bladder tumo
22	1034	51.9	6321	24	Human DNA sequence
23	1020	51.2	1685	11	Sequence encoding
24	1007	50.6	814	22	Human polynucleoti
25	963.5	48.4	1837	20	Human normal uteru
26	963.5	48.4	2078	20	Human normal ovari
27	963.5	48.4	2119	23	DNA encoding novel
28	949	47.6	1026	17	Human recombinant
29	949	47.6	2063	23	Human prostate exp
30	949	47.6	2063	23	Human prostate exp
31	949	47.6	2063	23	Human prostate exp
32	949	47.6	2063	23	Human prostate exp
33	948	47.6	2063	23	Human prostate exp
34	948	47.6	4167	21	CDNA encoding a ch
35	947	47.5	1002	14	Mature decorin PR-
36	947	47.5	4192	17	Collagen A1/decori
37	907	45.5	1593	11	Sequence encoding
38	906.5	45.5	1997	24	CDNA sequence #355
39	863.5	43.3	1854	22	Osteoarthritis tis
40	847	42.5	924	14	Decorin (N-termina
41	788.5	39.6	1674	22	DNA encoding human
42	776	39.0	849	14	Decorin (N-termina
43	616	30.9	711	14	Decorin (N-termina
44	608	30.5	496	22	Human differential
45	497.5	25.0	505	24	Target canine gene

ALIGNMENTS

RESULT 1
AA80043
ID AAX80043 standard; cDNA; 2454 BP.
XX AAX80043;
AC AAX80043;
DT 12-AUG-1999 (first entry)
XX Human PRO241 nucleotide sequence.
XX Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
KW secreted protein; transmembrane protein; inflammation disorder; ss.
XX Homo sapiens.
XX WO9928462-A2.
XX 10-JUN-1999.
PD


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XX 01-DEC-1998; 98WO-US25108.
XX
XX 25-FEB-1998; 98US-0075945.
XX 03-DEC-1997; 97US-0067411.
XX 11-DEC-1997; 97US-0069278.
XX 11-DEC-1997; 97US-0069334.
XX 11-DEC-1997; 97US-0069335.
XX 12-DEC-1997; 97US-0069425.
XX 16-DEC-1997; 97US-0069694.
XX 16-DEC-1997; 97US-0069696.
XX 16-DEC-1997; 97US-0069702.
XX 17-DEC-1997; 97US-0069870.
XX 17-DEC-1997; 97US-0069873.
XX 18-DEC-1997; 97US-0068017.
XX 05-JAN-1998; 98US-0070440.
XX 09-FEB-1998; 98US-0074086.
XX 09-FEB-1998; 98US-0074092.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Chen J, Goddard A, Gurney AL, Wood WI;
XX Yuan J;
XX
XX WPI; 1999-371118/31.
XX P-PSDB; AAY17820.
XX
XX Nucleic acids encoding PRO secreted and transmembrane proteins
XX
XX Claim 2; Fig 1; 123pp; English.
XX
XX The present invention describes nucleic acids encoding PRO secreted and
XX transmembrane proteins used therapeutically. The PRO proteins have
XX cytosstatic, anti-inflammatory, anti-proliferative and immunosuppressive
XX activity. The proteins and polynucleotides can be used in therapy,
XX identification of homologues, raising antibodies and design of probes
XX and primers. They can be used in a range of diseases related to proteins
XX that they have homology with, e.g. a PRO protein having homology to
XX complement proteins may be used in inflammatory responses.
XX
XX Sequence 2454 BP; 835 A; 432 C; 417 G; 770 T; 0 other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 7.16e-199 Length: 2454
XX Score: 1992.00 Matches: 379
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 20 Gaps: 0
XX
XX
XX 11S-09-944-884-2 (1-379) x AAX80043 (1-2454)
XX
XX 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPheSer 20
XX |||||
XX 234 ATGAAGAGATGATGCTCCTATTATCTGCTTTGTCTCTGCCAAACCCCTCTTTAGC 293
XX |||||
XX 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40
XX |||||
XX 294 CCTTCACATCGCACTGAAGATATGATGCTGAAGGATATGGAAGACACATGATGAT 353
XX |||||
XX 41 AspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60
XX |||||
XX 354 GATCATGATGATGATGATGATGATCATGATCAGGACAACTCTCTTTTCCAAACAAGAG 413
XX |||||
XX 61 ProArgSerHisPheProPheAspLeuPheProMetCysProPheGlyCysGlnCys 80
XX |||||
XX 414 CCAAGAAGCCATTTTTCATTTGATCTGTTTCCAAATGTGTCCATTTGGATGTCAGTGC 473
XX |||||
XX 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100
XX |||||
XX 474 TATTTCAGAGTGTATCATGCTGCATGATTTAGTTTGACTTCAGTCCCAACCAACATTCCA 533
XX |||||
XX 101 PheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluIleLysGluAsnAsp 120
XX |||||

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XX	07-JUN-2001.	
PD		
XX		
PF	01-DEC-2000; 2000WO-US32678.	
XX		
XX	01-DEC-1999; 99WO-US28301.	
PR	01-DEC-1999; 99WO-US28634.	
PR	02-DEC-1999; 99WO-US28551.	
PR	02-DEC-1999; 99WO-US28564.	
PR	02-DEC-1999; 99WO-US28565.	
PR	09-DEC-1999; 99US-0170262.	
PR	16-DEC-1999; 99WO-US30095.	
PR	20-DEC-1999; 99WO-US30911.	
PR	20-DEC-1999; 99WO-US30999.	
PR	30-DEC-1999; 99WO-US31243.	
PR	06-JAN-2000; 2000WO-US00277.	
PR	06-JAN-2000; 2000WO-US00376.	
PR	11-FEB-2000; 2000WO-US03565.	
PR	18-FEB-2000; 2000WO-US04341.	
PR	18-FEB-2000; 2000WO-US04342.	
PR	22-FEB-2000; 2000WO-US04414.	
PR	24-FEB-2000; 2000WO-US04914.	
PR	24-FEB-2000; 2000WO-US05004.	
PR	01-MAR-2000; 2000WO-US05601.	
PR	20-MAR-2000; 2000WO-US07377.	
PR	21-MAR-2000; 2000WO-US07532.	
PR	30-MAR-2000; 2000WO-US08439.	
PR	17-MAY-2000; 2000WO-US13705.	
PR	22-MAY-2000; 2000WO-US14042.	
PR	30-MAY-2000; 2000WO-US14941.	
PR	02-JUN-2000; 2000WO-US15264.	
PR	10-NOV-2000; 2000WO-US30873.	
XX		
XX	(GETH) GENENTECH INC.	
XX		
PI	Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;	
PI	Cerriksen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;	
PI	Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;	
XX		
XX	WPI: 2001-408281/43.	
DR	P-PSDB; AAU12335.	
DR		
XX	Isolated, secretory and transmembrane PRO polypeptide used to detect	
XX	other PRO polypeptides, link bioactive molecules to cells expressing	
PT	PRO polypeptides, and detect the presence of mammalian tumours e.g.	
PT	lung, breast, prostate, cervical	
PS	Claim 3; Fig 327; 813pp; English.	
XX		
CC	AAS21244-AAS21518 encode for novel human secretory and transmembrane	
CC	PRO polypeptides. The PRO polypeptides are useful to detect other	
CC	PRO polypeptides, to link bioactive molecules to cells expressing	
CC	PRO polypeptides, to modulate biological activities of cells expressing	
CC	PRO polypeptides, and to detect the presence of mammalian lung, colon,	
CC	breast, prostate, rectal, cervical or liver tumours by comparing PRO	
CC	polypeptide expression in a cell sample to that in a control sample.	
CC	Some of the 275 sequences are also useful to stimulate the release of	
CC	tumour necrosis factor-alpha (TNF-alpha) from human blood, the	
CC	proliferation or differentiation of chondrocytes, the proliferation or	
CC	gene expression in pericyte cells, the release of proteoglycans from	
CC	cartilage, the proliferation of inner ear utricular supporting cells or	
CC	of T-lymphocytes, the release of a cytokine from peripheral blood	
CC	monocytes (PBMCs), or the proliferation of endothelial cells. Some of	
CC	the PRO polypeptides may modulate glucose or free fatty acid uptake by	
CC	skeletal muscle cells or by adipocytes; or inhibit binding of a-peptide	
CC	to factor VIIA. The PRO polypeptides can be used in assays to identify	
CC	molecules involved in binding interactions. The polynucleotides encoding	
CC	PRO polypeptides can be used to generate probes, antisense RNA/DNA,	
CC	transgenic or knock out animals and can be used in gene therapy.	
XX		
SQ	Sequence 2454 BP; 835 A; 432 C; 417 G; 770 T; 0 other;	

Alignment Scores:

QY 321 AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys 340
 DB 1194 AATTCATTCAGAGAGGGAGTAATGACTTCTGTCACACAGTGCACAAAGATGAAGAAA 1253
 QY 341 SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnPro 360
 DB 1254 TCATTATACAGTGCATTAAGTTTATTCAACAACCCGGTGAATACGTGGAAATGCAACCT 1313
 QY 361 AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet 379
 DB 1314 GCAACATTCGTGTTGTTTGACAGCAATCAGTGTTTCAGCTTGGAACTTTTGAATG 1370

RESULT 3
 ABL95575
 ID ABL95575 standard; cDNA; 2454 BP.
 XX AC ABL95575;
 XX DT 19-JUL-2002 (first entry)
 XX DE Human angiogenesis related cDNA PRO241 SEQ ID NO: 29.
 XX KW Human; angiogenesis: PRO protein; cardiovascularisation; wound; cancer;
 XX OS atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 XX PN cardiant; cyostatic; antiangiogenic; hypotensive; vulnerary;
 XX PN antiarteriosclerotic; gene; ss.
 XX OS Homo sapiens.
 XX PN W0200208284-A2.
 XX PD 31-JAN-2002.
 XX PF 09-JUL-2001; 2001WO-US21735.
 XX PR 20-JUL-2000; 2000US-219556P.
 XX PR 25-JUL-2000; 2000US-220624P.
 XX PR 25-JUL-2000; 2000US-220664P.
 XX PR 28-JUL-2000; 2000WO-US20710.
 XX PR 02-AUG-2000; 2000US-222695P.
 XX PR 17-AUG-2000; 2000US-0643657.
 XX PR 23-AUG-2000; 2000WO-US23522.
 XX PR 24-AUG-2000; 2000WO-US23328.
 XX PR 07-SEP-2000; 2000US-230978P.
 XX PR 15-SEP-2000; 2000US-000000P.
 XX PR 18-SEP-2000; 2000US-0664610.
 XX PR 18-SEP-2000; 2000US-0665350.
 XX PR 24-OCT-2000; 2000US-242922P.
 XX PR 08-NOV-2000; 2000US-0709238.
 XX PR 08-NOV-2000; 2000WO-US30952.
 XX PR 10-NOV-2000; 2000WO-US30873.
 XX PR 01-DEC-2000; 2000WO-US32678.
 XX PR 20-DEC-2000; 2000US-0747259.
 XX PR 20-DEC-2000; 2000WO-US34956.
 XX PR 22-JAN-2001; 2001US-0767609.
 XX PR 28-FEB-2001; 2001US-0796498.
 XX PR 01-MAR-2001; 2001WO-US06520.
 XX PR 05-MAR-2001; 2001US-0802706.
 XX PR 14-MAR-2001; 2001US-0808689.
 XX PR 22-MAR-2001; 2001US-0816744.
 XX PR 05-APR-2001; 2001US-0828366.
 XX PR 10-MAY-2001; 2001US-0854208.
 XX PR 10-MAY-2001; 2001US-0854280.
 XX PR 25-MAY-2001; 2001US-0866028.
 XX PR 25-MAY-2001; 2001WO-US17092.
 XX PR 25-MAY-2001; 2001US-0866034.
 XX PR 30-MAY-2001; 2001US-0870574.
 XX PR 30-MAY-2001; 2001WO-US17443.
 XX PR 01-JUN-2001; 2001WO-US17800.
 XX PR 20-JUN-2001; 2001WO-US19692.
 XX PR 28-JUN-2001; 2001WO-US00000.

(GETH) GENENTECH INC.
 PA (BAKE) BAKER K P.
 PA (FERR) FERRARA N.
 PA (GERB) GERBER H.
 PA (GERR) GERITSEN M E.
 PA (GODD) GODDARD A.
 PA (GODO) GODOWSKI P J.
 PA (GURN) GURNEY A L.
 PA (HILL) HILLAN K J.
 PA (MARS) MARSTERS S A.
 PA (PANJ) PAN J.
 PA (PAON) PAONI N F.
 PA (STEP) STEPHAN J F.
 PA (WATA) WATANABE C K.
 PA (WILL) WILLIAMS P M.
 PA (WOOD) WOOD W I.
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI: 2002-171999/22.
 DR P-PSDB; ABB95437.
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX Claim 1; Fig 29; 567pp; English.
 PS The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a coding sequence of the invention.
 XX Sequence 2454-BP; 835 A; 432 C; 417 G; 770 T; 0 other;
 SQ

Alignment Scores:
 Pred. No.: 7.16e-199 Length: 2454
 Score: 1992.00 Matches: 379
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-09-944-884-2 (1-379) x ABL95575 (1-2454)

QY 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPheSer 20
 DB 234 ATGAAGGATGATGCTCTCTATTTATTCCTGGCTTGTGCTCTGCCAACCCCTTTTACG 293
 QY 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40
 DB 294 CCTTCACACATCGCACTGAAGATATGATGCTGGAAGATATGGAACACACAGATGATGAT 353
 QY 41 AspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60
 DB 354 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413
 QY 61 ProArgSerHisPhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 80
 DB 414 CCAAGAAGCCATTTTTCATTTGATCTGTTTCCCAATGTGTCATTTGATGATGATGATGATGAT 473
 QY 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100
 DB 474 TATTACAGATTGTACATGCTCAGATTAGTTGACCTCAGTCCACCAACACATTCAC 533
 QY 101 PheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluLysLysGluAsnAsp 120

XX SQ Sequence 2454 BP; 835 A; 432 C; 417 G; 770 T; 0 other;

Alignment Scores:

Pred. No.: 7.16e-199 Length: 2454

Score: 1992.00 Matches: 379

Percent Similarity: 100.00% Conservations: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 24 Gaps: 0

US-09-944-884-2 (1-379) x ABL88086 (1-2454)

QY 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLeuLysProPhePheSer 20
 DB 234 ATGAAGAGATGCTCTCTTATTTCTGCTTTGCTGCTGCAACCCCTCTTTAGC 293

QY 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40
 DB 294 CCTTCACATCGCACTGAACAATATGATGCTGAGGATATGGAGACACACATGATGAT 353

QY 41 AspAspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60
 DB 354 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413

QY 61 ProArgSerHisPhePheProPheAspLeuPheProMetCysPropheGlyCysGlnCys 80
 DB 414 CCAAGAAGCCATTTTTCATTTGATGCTGTTTCCAAATGTCCTGATGTCAGTGC 473

QY 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100
 DB 474 TATTCACGAGTGTACATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 533

QY 101 PheAspThrArgMetLeuAspLeuGlnAsnLysIleLysGluIleLysGluAsnAsp 120
 DB 534 TTTGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 593

QY 121 PheLysGlyLeuThrSerLeuTyrGlyLeuLeuLeuAsnAsnLysLeuThrLysIle 140
 DB 594 TTTAAAGGACTTCCTTCACTTTATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 653

QY 141 HisProLysAlaPheLeuThrThrLysLysLeuArgGluLeuThrSerHisAsnGln 160
 DB 654 CACCCAAAAGCTTCTTAACCAACAAGAGTTCGAAGGCTGATGCTGCTCCACAATCAA 713

QY 161 LeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180
 DB 714 CTAAGTGAATATACCACTTAATCTTCCCAATCATTAGCAGAACTCAGAAATTCATG 773

QY 181 LysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGlu 200
 DB 774 AAAGTTAAGAAATACAAAAGGACACATTCAGGAATGAATGCTTTTACACGTTTGGAA 833

QY 201 MetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThr 220
 DB 834 ATGAGTGCACCTCTTGTATATATGATGATGATGATGATGATGATGATGATGATGAT 893

QY 221 ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProPro 240
 DB 894 GTGTTCCATATACGAATTCAGAGCAAGCAAACTGACCTCAGTTCTTAAAGGCTTACC 953

QY 241 ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe 260
 DB 954 ACTTTATGAGGCTTCACTTAGATATATATAAATTTCAACAGTGGAACTTGGAGATTT 1013

QY 261 LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280
 DB 1014 AAAGTACAAAGCACTACAAAGGCTGGGCTAGGAACAAACAAATACAGATATCGAA 1073

QY 281 AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnAsnLysLeu 300
 DB 1074 AATGGGAGTCTGCTAACATACCACTGCTGAGAGAAATACATTTGGAAACATAACTA 1133

QY 301 LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSer 320
 DB 1134 AAAAAATCCCTTCAGGATTACCAGATTGAAATACCTCCAGATAATCTTCTTCATTCT 1193

QY 321 AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys 340
 DB 1194 AATTCATTTGCAAGAGTGGGAGTAATGACTTCTGTCCAACAGTCCCAAGATGAAGAA 1253

QY 341 SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnPro 360
 DB 1254 TCTTTATACAGTGCATTAAGTTTATTCAACACCCGGTGAATACTGGGAATGCAACT 1313

QY 361 AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet 379
 DB 1314 GCAACATTTGCTGTGTTTGGAGCAATGAGTGTTCAGCTTGGGAACCTTTGGAATG 1370

RESULT 5
 AAA49551 standard; cDNA; 2455 BP.
 XX AAA49551;
 AC AAA49551;
 DT 25-SEP-2000 (first entry)
 XX Human PRO241 cDNA.
 KW PRO: membrane bound protein; secreted protein; PRO357; PRO327;
 KW PRO243; PRO715; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347;
 KW PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide;
 KW antibody; screening; detection; inhibition; probe; primer; human;
 ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 234..1373
 FT /*tag= a
 FT /product= PRO241 polypeptide
 XX WO200032776-A2.
 XX 08-JUN-2000.
 PF 01-DEC-1999; 99WO-US28301.
 XX 01-DEC-1998; 98WO-US25108.
 PR 16-DEC-1998; 98US-0112850.
 PR 22-DEC-1998; 98US-0113296.
 XX (GETH) GENENTECH, INC.
 FA Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
 XX Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
 PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
 XX WPI; 2000-412324/35.
 DR P-PSDB; AAB01311.
 XX New human nucleic acids encoding secreted and transmembrane
 PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical
 PT and diagnostic agents
 XX Claim 2; Fig 1; 187pp; English.
 CC New human nucleic acids encoding secreted and transmembrane
 CC polypeptides which are designated as PRO polypeptides are described
 CC The membrane-bound proteins have various industrial applications,
 CC including as pharmaceutical and diagnostic agents. The membrane-bound
 CC proteins can also be employed for screening of potential peptide or
 CC small molecule inhibitors of the relevant receptor/ligand interaction.
 CC Anti-PRO antibodies are useful for the affinity purification of PRO
 CC from recombinant cell culture or natural sources.
 XX

SQ Sequence 2455 BP; 836 A; 432 C; 417 G; 770 T; 0 other;

Alignment Scores:
Pred. No.: 7,16e-199 Length: 2455
Score: 1992.00 Matches: 379
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 21 Gaps: 0

US-09-944-884-2 (1-379) x AAA49551 (1-2455)

Qy 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPhePheSer 20
|||||
Db 234 ATGAAGGAGTATGTCTCCATTATTTCCTGGCTTTTGCTCTCGCAAAACCCCTCTTAGC 293
|||
21 ProSerHisLeuAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40
|||||
294 CCTTCACATCCCATCGAAGTAATGATGCTGAAGGATATGGAAGACACAGATGATGAT 353
|||||
Qy 41 AspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60
|||||
Db 354 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413
|||||
Qy 61 ProArgSerHisPhePheProPheLeuPheProMetCysProPheGlyCysGlnCys 80
|||||
Db 414 CCAAGAAGGCCATTTTTTCCATTTGATCTGTGTTCCAAATGTGCCATTTGGATGTCAGTGC 473
|||||
Qy 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100
|||||
Db 474 TATTACAGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 533
|||||
Qy 101 PheAspThrArgMetLeuAspLeuGlnAsnAsnLysLysLysLysLysLysLysLysLys 120
|||||
Db 534 TTGTACTCGATGCTGTGATCTTCAACAATAAATAAATAAATAAATAAATAAATAAATCAT 593
|||||
Qy 121 PheLysGlyLeuThrSerLeuThrGlyLeuLeuLeuAsnAsnLysLeuThrLysIle 140
|||||
Db 594 TTTAAAGGACTCACTTCACTTTATGCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 653
|||||
Qy 141 HisProLysAlaPheLeuThrThrLysLysLeuArgArgLeuThrLysSerHisAsnGln 160
|||||
Db 654 CACCACAAAAGCCCTTCAACCAAGAAAGATGGCAAGGCTGTATCTGTCCCACAAATCAA 713
|||||
Qy 161 LeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180
|||||
Db 714 CTAAAGTGAATACCACTTAATCTCCCAATCATATAGCAGAACTCAGAAATCATCAAAAT 773
|||||
Qy 181 LysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGlu 200
|||||
Db 774 AAAGTTAAGAAAAATACAAAGGACACATTCAAAGGAATGAATGCTTTACACGCTTTGGAA 833
|||||
Qy 201 MetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheCluclyValThr 220
|||||
Db 834 ATGAGTCAAACCCCTTGTATAATATGAGGATAGCCAGGGGCAATTTGAAGGGGTGAGC 893
|||||
Qy 221 ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProPro 240
|||||
Db 894 GTGTTCCATATCAGATTCGAGAGCAAAACCTCACCTCAGTTCCTAAAGGCTTACCACCA 953
|||||
Qy 241 ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValcLuLeuGluAspPhe 260
|||||
Db 954 ACTTTATTGGAGCTTCATTTAGATTATATAAATTTCAACAGTGGAACTTCAGGATTTT 1013
|||||
Qy 261 LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280
|||||
Db 1014 AAACGATPACAAAGAACTACAAAGGCTGGGCTAGGAAACAAACAAATACAGATATCGAA 1073
|||||
Qy 281 AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnAsnLysLeu 300
|||||
Db 1074 AATGGGAGCTTCTGATACATACACAGCTGTGAGAGAAATACATTTGGAAACAAATAACTA 1133
|||||
Qy 301 LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSer 320
|||||

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technology to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting and quantitating a polypeptide in tissue, as molecular weight markers and as

a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention. CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 1492 BP; 499 A; 279 C; 279 G; 435 T; 0 other;

Alignment Scores:

Pre-d. No.: 5,896-182 Length: 1492
e: 1828.00 Matches: 374
Sent Similarity: 96.41% Conservative: 2
Best Local Similarity: 95.90% Mismatches: 2
Query Match: 91.77% Indels: 12
DB: 23 Gaps: 1

US-09-944-884-2 (1-379) x AAS86756 (1-1492)

QY 2 LysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPhe-PheSerP 21
Db 236 AAGGAGTATGCTCCTAATTATTCCTGGCTTGTGCTCTGCCAAACCTTCTTGGCC 295
QY 21 roSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetClnuAspThrAspAspA 41
Db 296 CTTACACATCGCCTGAAGATATGATGCTGAAGATATGGAACACACAGATGAGG 355
QY 41 sp-----AspAspAspAspAspAspAspAspAspAspAspAspSerLeuPheProThra 59
Db 356 ATGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 415
QY 59 rgGluProArgSerHis-PhePheProPheAspLeuPhePrometCysProPheGlyCys 78
Db 416 GAGAGCCCAAGAGCCATTTTTCCTATTTGATCTGTTTCCCAATGTCCTCATTTGGATGT 475
QY 79 GlnCysTyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsn 98
Db 476 CAGTGTCTATTCAGAGTGTACATTTGCTCAGATTTAGTTTGCACCTCAGCTCCCAACCAAC 535
QY 99 IleProPheAspThrArgMetLeuAsnAsnLysIleLysGluIleLysGlu 118
Db 536 ATTCATTGTGACTCGAATGCTTCAATCAACATATAAATTAAGGAATCAAGNA 595
QY 119 AsnAspPheLysGlyLeuThrSerLeuTyrGlyLeuIleLeuAsnAsnLysLeuThr 138
Db 596 AATGATTTTAAAGGACTCACTTCACCTTTATGCTCTGATCTCGATCCTGAACAACAAGCTAACG 655
QY 139 LysIleHisProLysAlaPheLeuThrLysLysLysLeuArgArgLeuTyrLeuSerHis 158
Db 656 AAGATTTCACCCAAAAGCCCTTCTAACCACAAAGAAGTTGCGAAGGCTGATCTGCTCCAC 715
QY 159 AsnGlnLeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHis 178
Db 716 AATCAACTAAGTGAATACCACTTAATCTTCCCAATCATATAGCAAGCTCAGAATTCAT 775
QY 179 GluAsnLysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisVal 198
Db 776 GAAATTAAGTTAAGAAATACAAAAGGACACATTCAAAGGAATGATGCTTTACACGTT 835
QY 199 LeuGluMetSerAlaAsnProLeu-AspAsnAsn-GlyIleGluProGlyAlaPhe--G1 217
Db 836 TTGGAAATCAGTGCACCAACCTCTTTGATATAATATGGGGATAGACGAGGGCATTTTGAA 895
QY 217 uGlyValThrValPheHisIleArgIleAlaGluAlaLysLeuThrSerVal-Pro-Lys 236
Db 896 GGGGTGACGGGTGTTCCATATCAGATTCAGAAATTCAGAAAGCAAACTGACCTCAGTTCTCTAAAG 955

QY 237 GlyLeuProProThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGlu 256
Db 956 GGCTTACCACCAACTTTATTGGAGCTTCACCTAGATTATAATAAAATTTCAACAGTGGAA 1015
QY 257 LeuGluAspPheLysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIle 276
Db 1016 CTTGAGGATTTTAAACGATACAAAGACTACAAAGCTGGCCCTAGGAAACACAAATC 1075
QY 277 ThrAspIleGluAsnGlySerLeuAlaAsnIleProArgValArg-GluIleHisLeuG1 296
Db 1076 ACAGATATCGAAATGGGAGTCTTGTCTAACATACCACTGTGAGGAGAGATACATTTGGG 1135
QY 296 uAsnAsnLysLeuLysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIle1 316
Db 1136 AAACATTAAACTAAATAAAATCCCTTCAGAGTATCCAGAGTTGAATACCTCCAGATAAT 1195
QY 316 ePheLeuHisSerAsnSerIleAlaArgValGlyValAsnAspPheCysProThrValPr 336
Db 1196 CTTCTTCATCTTAATCAATGCAAGAGTGGAGTAATACCTCTCTCCACAGTCC 1255
QY 336 oLysMetLysLysSerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTr 356
Db 1256 AAAGATGAAGAAATCTTTATACAGTGCATAAAGTTTATTCAACACCCCGGTGAATACTG 1315
QY 356 pGluMetClnProAlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAs 376
Db 1316 GGAAATGCAACCTGCAACATTTCTGTTGTGTTGAGCAGAATGAGTGTTCAGCTGGGAA 1375
QY 376 nPheGlyMet 379
Db 1376 CTTTGGCAATG 1385
RESULT 8
AADI0114
ID AADI0114 standard; cDNA; 2305 BP.
XX AADI0114;
AC AADI0114;
XX 12-SEP-2001 (first entry)
DT Mouse bone/cartilage proteoglycan I (BGN) cDNA.
DE Mouse; cytotatic; antiinflammatory; immunoregulatory; tissue integrity;
KW wound healing; immune response; vaccine; cancer; asthma; allergy;
KW cell trafficking; BGN; bone/cartilage proteoglycan I protein;
KW biglycan; PG-SI; secreted protein; therapy; ss.
OS Mus sp.
FH Key Location/Qualifiers
FT CDS 238..1359
FT /*tag= a
FT /product= *Mouse bone/cartilage proteoglycan I*
XX WO200148192-A1.
PN 05-JUL-2001.
XX 21-DEC-2000; 2000WO-NZ00256.
PF 23-DEC-1999; 99US-0171678.
PR 28-NOV-2000; 2000US-0724864.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX Watson, JD, Murison JG;
PI WPI; 2001-425665/45.
DR P-PSDB; AAE05347.
XX Novel isolated polypeptide useful to isolate corresponding interacting
PT proteins or other compounds, to quantitatively determine levels of
PT interacting proteins or other compounds, and as therapeutic target

XX Claim 1; Page 53.55; 101pp; English.

XX The patent discloses novel polynucleotides and their corresponding proteins which play a major role in induction of growth, cell migration and proliferation, cell-cell interaction and the differentiation of tissue-specific cells. These proteins are important in the maintenance of tissue integrity and thus are important in wound healing. They are useful in various assays to determine the biological activity, to raise antibodies, to isolate corresponding interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or other compounds, and as therapeutic target in a whole range of disease states. Compositions comprising the novel proteins of the invention are useful for treating mammalian disorders. Polynucleotides of the invention are useful in genome and physical mapping, in positional cloning of genes, to tag or identify an organism or its reproductive material (as non-disruptive tags for marking organisms), and for the diagnosis and treatment of mammalian diseases which is the consequence of inappropriate expression of kinase genes. They are useful for promoting immune response as part of a vaccine or anti-cancer treatment, as target for cancer treatment, as immunoregulatory and anti-inflammatory molecule, as diagnostic for specific types of cancer and for development of an anti-cancer treatment, and as a target for antagonists in the treatment of diseases such as asthma and allergy. They are also useful to inhibit or enhance the activity of the soluble molecule that binds proteins of the invention, for tissue and neural regeneration, to promote or block cell trafficking, and as anti-inflammatory and/or vaccine adjuvant. The present sequence is a cDNA encoding bone/cartilage proteoglycan I protein (BGN), a secreted protein from mouse. BGN is also known as biglycan or PG-S1.

SQ Sequence 2305 BP; 809 A; 395 C; 391 G; 710 T; 0 other;

Alignment Scores:

Pred. No.: 1.19e-178 Length: 2305
Score: 1799.00 Matches: 341
Percent Similarity: 94.71% Conservative: 17
Best Local Similarity: 90.21% Mismatches: 14
Query Match: 90.31% Indels: 6
DB: 22 Gaps: 1

US-09-944-884-2 (1-379) x AAD10114 (1-2305)

QY 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPhePheSer 20
|||||
DB 238 ATGAGGAGTATGCTACTGCTTTGGCTGTGTCTGCTGCCAAACCTCTCTTAC 297
QY 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40
|||||
DB 298 CCTTCCCACAGCAGCAGTGAAGATATGATGTTGAAGGATATGGAAGACACAGATGATGAC 357
41 AspAspAspAspAspAspAspGluAspAspGluAspAspSerLeuPheProThrArgGlu 60
|||||
DB 358 GATACGATGATGAC-----GACAACTCTCTTTTCCACGAAGAG 399
QY 61 ProArgSerHisPhePheProPheAspLeuPheProMetCysProPheCysGlnCys 80
|||||
DB 400 CCAGTGAACCTTTTCCCTTCGATTTGTTCCAAATGTCCTATTTGGGTGCCAATGT 459
QY 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100
|||||
DB 460 TACTCTCGAGTGTTCCTGCTCTGATCTAGTCTGACATCGGTTCACAAACATCCCA 519
QY 101 PheAspThrArgMetLeuAspLeuGlnAsnLysIleLysGluIleLysGluAsnAsp 120
|||||
DB 520 TTTGATCTCGAATGTTGACCTTCAAAATATAAATCAAGGAATTAAGAAATGAC 579
QY 121 PheLysGlyLeuThrSerLeuTyrGlyLeuLeuLeuAsnAsnLysLeuThrLysIle 140
|||||
DB 580 TTTAAGGACCTCACTTCTGATCTGATCTGAAACAAACAAAGCAAGATTAAGAAAT 639
QY 141 HisProLysAlaPheLeuThrLysLysLeuArgArgLeuTyrLeuSerHisAsnGln 160
|||||

DB 640 CACCACAAACCTTTCTTAACCAAGAAATTTGAGAGGCTATATTTATCCCAACCA 699
QY 161 LeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180
|||||
DB 700 CTAAGTGAATTCACCTTAATCTTCCCAATCATTTAGCAGAACTCAGAAATCATGATA 759
QY 181 LysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGlu 200
|||||
DB 760 AAGTTAAGAAGATACAAAGACACGTTCAAGGAATGAATGCTTTTACATGTTTGA 819
QY 201 MetSerAlaAsnProLeuAspAsnGlyIleGluProGlyAlaPheGluGlyValThr 220
|||||
DB 820 ATGAGTGAACCTCTTGAAGAACACCGGATGAACCGGGCATTTCAAGGGGTGACA 879
QY 221 ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuPro 240
|||||
DB 880 GTATTCCATATCAGGATCGCTGAACAACTCACTCAATTCACAAAGGCTTACCACCA 939
QY 241 ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe 260
|||||
DB 940 ACTTTGCTGGAGCTTCATTAGATTTTAATAAAATTTCAACGGTGAACCTTGAGACT 999
QY 261 LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280
|||||
DB 1000 AAACGTCAGGGAACCTGCAAGGCTGCTTGGAAACACAGAAATCACAGATATTGAA 1059
QY 281 AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnAsnLysLeu 300
|||||
DB 1060 AATGCAACTTTTGCTAATATATACCGCTGTGAGAGATACACTTGGACACAAATAACTA 1119
QY 301 LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSer 320
|||||
DB 1120 AAAAAATCCCTTCAGGAGTTGAATACCTCCAGATAATCTTCCTTCATAT 1179
QY 321 AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys 340
|||||
DB 1180 AATTCATTTGCAAAAGTGGAGTGAATGACTTCTGTCCACAGCTGCCAAGATGAAGAA 1239
QY 341 SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnPro 360
|||||
DB 1240 TCTTTATACAGTGCATAAAGTTTATTCAACCAACCAATGAAGTACTGGGAAATACAAC 1299
QY 361 AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGly 378
DB 1300 GCAACATTTCTGTGTGTTCTTTGGCAGAAATGAGTGTTCAGCTTGGGAATGTTGA 1353
RESULT 9
ABL35045
ID ABL35045 standard; cDNA; 2305 BP.
XX
AC ABL35045;
XX
DT 04-APR-2002 (first entry)
XX
DE Murine cDNA isolated from skin cells SEQ ID NO: 574.
XX Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
KW developmental defect; inflammatory disease; dermatological; vulnery;
KW immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
SS.
XX Mus sp.
XX WO200190357-A1.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-N200099.
XX
PR 24-MAY-2000; 2000US-206650P.
XX
PR 25-JUL-2000; 2000US-221232P.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.

Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD; WPI; 2002-122020/16. P-PSDB; ABB72356.

New polynucleotides and polypeptides encoded by the polynucleotides isolated from skin cells, useful for treating skin wounds, cancers, PT growth and developmental defects, inflammatory diseases, or for PT modulating immune responses

Claim 1; Page 359; 466pp; English.

The present invention provides the protein and coding sequences of cDNAs CC isolated from human, murine and rat skin cell libraries. The sequences CC can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound healing and in modulating immune responses. The present sequence is a CC cDNA of the invention.

Sequence 2305 BP; 809 A; 395 C; 391 G; 710 T; 0 other;

Alignment Scores:

Pred. No.:	Length:	Matches:
Score:	1,19e-178	2305
Percent Similarity:	94.71%	341
Best Local Similarity:	90.21%	Mismatches: 14
Query Match:	90.31%	Indels: 6
DB:	24	Gaps: 1

US-09-944-884-2 (1-379) x ABL35045 (1-2305)

Qy 1 MetLysGLuTyrValLeuLeuPheLeuAlaLeuCysSerAlaLysProPheSer 20
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 238 ATGAAGAGATGTGATGCTACTGCTTTGGCTGTGTGCTCTGCCAAACCCCTCTTTAGC 297

Qy 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 298 CCTTCCCACACAGCACTGAAGAATATGATTGTGAAGGATATGGAAGACACAGATGATGAC 357

Qy 41 AspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProthrArgGlu 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 358 GATAACGATGATGAC-----GACAACCTCTCTTTTCCAACGAAAGAG 399

Qy 61 ProArgSerHisPhePheProPheAspLeuPheProMetCysProPheGlyCysGlnCys 80
| | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 400 CCAGTGAAACCCTTTTTCCTTCGATTTGTTTCCAACATGTCATTTGGTGCCTAATGT 459

Qy 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProthrAsnIlePro 100
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 460 TACTCTCGAGTGTTCCTGCTCTCATCTAGCTCTGACATCGGTGCCAACACATGCCA 519

Qy 101 PheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluIleLysGluAsnAsp 120
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 520 TTTCGATCTCGAATGGTTGACCTTCAAATAATAAAATCAAGAAATTAAGAAATGAC 579

Qy 121 PheLysGlyLeuThrSerLeuTyrGlyLeuIleLeuAsnAsnLysLeuThrLysIle 140
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 580 TTTAAAGGACTCACCTTCACTTTATGCTCTGATTTCTGAACAACAACAAGCTAACAAAAGATT 639

Qy 141 HisProLysAlaPheLeuThrThrLysLysLeuArgArgLeuTyrLeuSerHisAsnGln 160
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 640 CACCCAAAAACCTTTCTTAACCAACAAGAAATGAGAAGGCTATATTTATCCCCAACACCAA 699

Qy 161 LeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 700 CTAGTGAATTCCTCACTTAAATCTTCCCAANTCATTAGCAGAACTCAGAATTCATGATAT 759

Qy 181 LysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGlu 200
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

Db	760	AAAGTTAAGAAGATACAAAGAGGACAGCTTCAACGGGAATGAATGCTTTACATGCTTTTGGAA	819
Qy	201	MetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThr	220
Db	820	ATGAGTGCRAACCTCTTGAGAACACAGGATAGAACAGGGCCATTTGAAGGGGTGACA	879
Qy	221	ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProPro	240
Db	880	GTATTCCATATCAGGATCGCTGAAGCAAAACTAACCTCAATTCCAAAGGCCCTACCACCA	939
Qy	241	ThrLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe	260
Db	940	ACTTTGCTGAGCTTCATTTAGATTTTAAATAAATTTCAACGGTGGACTTGAAGATCTT	999
Qy	261	LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnLysIleThrAspIleGlu	280
Db	1000	AAACGGTACAGGGAAGCTGCAAAGGCTGGGTCTTTGGAAACAACAGAAATCACAGATATTGAA	1059
Qy	281	AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnAsnLysLeu	300
Db	1060	AATGGAACTTTTGTCTATATATACCACGCTGTGAGAGAGATACACTTGGAAACAATAAACTA	1119
Qy	301	LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSer	320
Db	1120	AAAAAATCCCTTCAGGATTCACAGGAGTTGAATATCTCCAGATAATCTTCCTTCATAT	1179
Qy	321	AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys	340
Db	1180	AATTCATTCGAAAAGTGGGAGTCAATGACTTCTGTCCACAGTGCACAAAGATGAAGAAA	1239
Qy	341	SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnPro	360
Db	1240	TCCTTATACAGTGCATAAGCTTTATTCAACAACCAATGAAGTACTCGGAAATACAACCT	1299
Qy	361	AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGly	378
Db	1300	GCAACATTTCCGTGTGTCTTCGGCAGATGAGTGTTCAGCTTGGCAATGTTGGA	1353
RESULT 10			
ID	AAH18405		
XX	AAH18405 standard; cDNA; 2089 BP.		
AC	AAH18405;		
XX	26-JUN-2001 (first entry)		
DT	Human cDNA sequence SEQ ID NO:18472.		
DE	Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.		
XX	Homo sapiens.		
OS	EP1074617-A2.		
PN	07-FEB-2001.		
XX	28-JUL-2000; 2000EP-0116126.		
PF	29-JUL-1999; 99JP-0248036.		
XX	27-AUG-1999; 99JP-0300253.		
PR	11-JAN-2000; 2000JP-0118776.		
PR	02-MAY-2000; 2000JP-0183767.		
PR	09-JUN-2000; 2000JP-0241899.		
XX	(HELI-) HELIX RES INST.		
PA	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;		
XX	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;		
PI	WPI; 2001-318749/34.		
XX	Primer sets for synthesizing polynucleotides, particularly the 5602		
PT	full-length cDNAs defined in the specification, and for the detection		

CC represent oligonucleoti

CC represent oligonucleoti

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CC of the present invention.
XX
SQ Sequence 854 BP; 281 A; 166 C; 162 G; 242 T; 3 other;

Alignment Scores:
Pred. No.: 5,33e-119 Length: 854
Score: 1225.00 Matches: 235
Percent Similarity: 96.33% Conservative: 1
Best Local Similarity: 95.92% Mismatches: 5
Query Match: 61.50% Indels: 4
DB: 22 Gaps: 1

US-09-944-884-2 (1-379) x AAI16847 (1-854)
QY 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPhePheSer 20
DB 92 ATCAAGGAGTATGTGCTCTATTATTCCTGGCTTGTCTGCCAACCCTTCTTTAGC 151
QY 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThr----- 37
DB 152 CCTTCACATCGCATCGAAGATATGCTGCTGAAGATATGGAAGACACAGATGATGAT 211
QY 38 ---AspAspAspAspAspAspAspAspAspAspGluAspAsnSerLeuPhe 56
DB 212 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 271
QY 57 ProThrArgGluProArgSerHisPhePhePhePhePhePhePhePhePhePhe 76
DB 272 CCAACAAGAGAGCAAGAACCCATTTTTCCTATTCATGCTGCTCAATGCTGCTCATTT 331
QY 77 GlyCysGlnCysTyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValPro 96
DB 332 GAGTGTGCTGCTATTCACAGGTGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 391
QY 97 ThrAsnIleProPheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluIle 116
DB 392 ACCAACATTCATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 451
QY 117 LysGluAsnAspPheLysGlyLeuThrSerLeuTyrGlyLeuIleLeuAsnAsnLys 136
DB 452 AAAGAAAATGATTTAAAGAGCTCACTTCATCTTATGCTGCTGCTGCTGCTGCTGCTGCT 511
QY 137 LeuThrLysIleHisProLysAlaPheLeuThrThrLysLysLeuArgArgLeuTyrLeu 156
DB 512 CTACGGAAGATTCACCAAAAGCCTTCTTACCAAAAGAGTTGCCAAGGCTGTATCTG 571
QY 157 SerHisAsnGlnLeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArg 176
DB 572 TCCCAACATCAACTAAGTGAATACCATTAATCTTCCCAATCATTAGCAGAACTCAGA 631
QY 177 IleHisGluAsnLysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeu 196
DB 632 ATTCATGAAATTAAGTTAAGAAAATACAAAGAGACACATTCAAAGGAATGAATGCTTTA 691
QY 197 HisValLeuGluMetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPhe 216
DB 692 CACGTTTGGAAATGATGCAACCCCTCTGTGATAAATGGGATAGCCAGGGGATTT 751
QY 217 GluGlyValThrValPheHisIleArgIleAlaIleAlaLysLeuThrSerValProLys 236
DB 752 GAAGGGTGCAGGTGTTCATATACAAATTCAGAAATTCAGAAAGCAAACTGGNCTCAGTTCCTAA 811
QY 237 GlyLeuProProThr 241
DB 812 GATAATCTTCCTTCA 826

RESULT 13:
AAT08768
ID AAT08768 standard; cDNA; 2446 BP.
XX
AC AAT08768;
XX
DT 20-MAR-1996 (first entry)

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XX Rat biglycan cDNA.
DE
XX
KW Biglycan; proteoglycan; chondroitin sulphate; neuron protection;
KW neurotrophic; central nervous system; CNS; memory loss; dementia;
KW learning; ss.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
CDS 123..1232
FT /*tag= a
FT sig_peptide 123..233
FT mat_peptide 234..1229
FT /*tag= b
FT /*tag= c
XX
PN W09530432-A1.
XX
PD 16-NOV-1995.
XX
PF 09-MAY-1994; 94WO-EP01479.
XX
PR 09-MAY-1994; 94WO-EP01479.
XX
PA (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX
PI Hasenoechrl R, Huston J, Junghans U, Kappler J, Koops A;
PI Mueller HW;
XX
PI WPI: 1995-403938/51.
XX
P-PSDB; AAR87951.
XX
PT Proteoglycan cpds., partic. chondroitin sulphate proteoglycan(s)
PT for maintain structural and function of the CNS and attenuating
PT memory deficit(s) in the elderly and patients with dementia
XX
PS Disclosure; Page 44-45; 60pp; English.
XX
CC A cDNA sequence (AAT08768) obtd. from rat smooth muscle codes for rat
CC biglycan (AAR87951), a chondroitin sulphate proteoglycan with
CC neurotrophic activity for brain neurons. The cDNA may be inserted
CC into a vector and used for prodn. of recombinant biglycan in
CC eukaryotic host cells.
XX
SQ Sequence 2446 BP; 562 A; 768 C; 508 G; 608 T; 0 other;

Alignment Scores:
Pred. No.: 5.28e-99 Length: 2446
Score: 1040.50 Matches: 199
Percent Similarity: 70.37% Conservative: 67
Best Local Similarity: 52.65% Mismatches: 93
Query Match: 52.23% Indels: 19
DB: 16 Gaps: 3

US-09-944-884-2 (1-379) x AAT08768 (1-2446)
QY 4 TyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPhe-----Phe 19
DB 135 TGCGTACTACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 194
QY 20 SerProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 39
DB 195 TGGGACTTCACCTTGGATGATGGGCTGCTCATGATGATGATGATGATGATGATGATGAT 254
QY 40 AspAspAspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArg 59
DB 255 GACACCACCTTCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 299
QY 60 GluProArgSerHisPhePhePhePhePhePhePhePhePhePhePhePhePhePhe 79
DB 300 -----TTTCAGTGGCCATGTGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 329

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Db 451 AAGGGTCTCCAGCAGCTTACGCCCTCGCTGGTGAACAACAGATCTCCAGATCCAT 510
QY 142 ProlysalapheLeuThrLysLysLeuArgLeuArgLeuSerHisAsnGlnLeu 161
Db 511 GAGAGGGCTTCAGCCCACTGCGGAAGCTGCAAGACTATCATCTCCAAGAACCACTG 570
QY 162 SerGluileProLeuAsnLeuProLysSerLeuAlaGluLeuArgileHisGluAsnLys 181
Db 571 GTGGAGATCCGCGCCCACTTACCACCTCCCTGGTGGAGCTCGGCATCCAGCAACACCGC 630
QY 182 ValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGluMet 201
Db 631 ATCCGGAAGTCCCAAGGAGGTTCAGCGGGCTCCGGAACATGACTCCATCGAGATG 690
QY 202 SerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThrVal 221
Db 691 GCGGGAACCCACTGGAGAACAGTGGCTTTGACCTGGAGCTTCGATGGCTGAAGCTC 750
QY 222 PheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProThr 241
Db 751 AACTACTCTGGCATCTCAGAGGCAAGCTGACTGGCATCCCAAGACCTCCCTGAGACC 810
Db 242 LeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPheLys 261
Db 811 CTGAATGAATCCACCTAGACCAACAATAATCCAGGCCATCGAATCGGAGGACCTGCTT 870
QY 262 ArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGluAsn 281
Db 871 CGTACTCAAGCTGTACAGGCTGGGCTAGGCCCTAGGCCACAGATGATGATGAGAAC 930
QY 282 GlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnAsnLysLeuLys 301
Db 931 GGGAGCTGAGTCTCTGCCACCTCCCGGAGCTCCACTTGGACAAACAAGTTGGCC 990
QY 302 LysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSerAsn 321
Db 991 AGGGTCCCTCAGGGCTCCAGACCTCAAGCTCTCCAGGTGTCTATCTGCACTCCAAC 1050
QY 322 SerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysSer 341
Db 1051 AACATCACCACCAAGTGGGTGTACACGACTTCTGTCCATGGGCTTCGGGGTGAAGCGGCC 1110
QY 342 LeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnProAla 361
Db 1111 TACTACAGGCATCAGCTCTTCAACAACCCCGTCCCTACTGGAGGTGACGCGGCC 1170
QY 362 ThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPhe 377
Db 1171 ACTTTCCGCTGGCTCACTGACCGCCTGGCCATCCAGTCTTGGCAACTAC 1218

JLT 15
...83977
ID AAF83977 standard; DNA; 1685 BP.
AC XX
XX XX
XX XX
DT 06-AUG-2001 (first entry)
XX XX
DE Human biglycan encoding nucleotide sequence.
XX XX
KW Dystrophin-associated protein complex; DAPC; postsynaptic membrane;
KW biglycan; muscular dystrophy; neuromuscular; neurological; smooth muscle;
KW nontropic; neuroleptic; antiviral; ds.
XX XX
OS Homo sapiens.
XX XX
FH Key
FT Location/Qualifiers
FT 121..1227
FT /*tag= a
XX XX
PN WO200136475-A2.
XX XX

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PD 25-MAY-2001.
XX XX
PF 17-NOV-2000; 2000WO-US31661.
XX XX
PR 18-NOV-1999; 99US-0166253.
XX XX
PA (UYBR-) UNIV BROWN RES FOUND.
XX XX
PI Fallon J, McKechnie B, Rafil M, Creely H, Bowe M, Ferri R;
XX XX
XX WPI; 2001-355617/37.
XX XX
XX P-PSDB; AAB85043.
XX XX
XX Stabilizing dystrophin-associated protein complexes and activating
XX postsynaptic membrane of a cell for treating or preventing muscular,
XX neuromuscular and neurological disorders, involves contacting cell with
XX biglycan
XX XX
PS Disclosure; Page 101-108; 112pp; English.
XX XX
XX The invention relates to stabilizing dystrophin-associated protein
XX complexes (DAPCs) on the surface of a cell or activating a postsynaptic
XX membrane of a cell that comprises contacting the cell with an effective
XX amount of biglycan. A composition comprising biglycan or its portion
XX is useful for treating or preventing a condition associated with abnormal
XX DAPC in cells, characterized by breakdown of muscle cell membrane, which
XX includes muscular dystrophies, such as Duchenne's, Becker's, Congenital,
XX limb-girdle muscular dystrophy and myotonic dystrophy and a condition
XX characterized by abnormal neuromuscular junction or synapse, such as
XX neuromuscular or neurological diseases in a subject. Neurological
XX disorders, include polymyositis and Alzheimer's disease. Biglycan is also
XX useful for preventing and treating smooth muscle disorders, such as
XX cardiac myopathies and for treating and inhibiting infections of cells by
XX microorganisms e.g. viruses. Agents that modulate the activity of
XX DAG-125, identified by the methods are useful in the prophylactic and
XX therapeutic treatments of diseases or disorders, characterized by an
XX unstable DAPC or an inappropriate formation of a postsynaptic
XX differentiation. Biglycans are also useful as a supplement to brain or
XX muscle cell or tissue culture and, tissues can be incubated in vitro
XX with biglycan to reverse tissue atrophy and to improve their growth or
XX survival in vitro. The present sequence represents a nucleotide sequence
XX encoding human biglycan.
XX XX
SQ Sequence 1685 BP; 357 A; 593 C; 436 G; 299 T; 0 other;

Alignment Scores:
Pred. No.: 1.52e-98 Length: 1685
Score: 1034.00 Matches: 200
Percent Similarity: 69.95% Conservative: 63
Best Local Similarity: 53.19% Mismatches: 93
Query Match: 51.91% Indels: 20
DB: 22 Gaps: 3

US-09-944-884-2 (1-379) x AAF83977 (1-1685)
QY 6 LeuLeuPheLeuAlaLeuLysSerAlaLysProPhe-----PheSerPro 21
Db 139 CTCGTGTCTCTGCTGGCCCTGAGCCAGCCCTTTCGAGCAGAGAGGCTTCTGGGAC 198
QY 22 SerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAspAsp 41
Db 199 TTCACCTCGAGCATGGGCCATTCATGATGACATGAGGAAGCTTCGGGGCTGACACC 258
QY 42 AspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGluPro 61
Db 259 TCAGGCGCTCTGGACCCGAC-----TCTGTACACACCCACCTACAGC--- 300
QY 62 ArgSerHisPhePhePheProPheAspLeuPheProMetCysProPheGlyCysGlnCysTyr 81
Db 301 -----GCCATGTGTCTTTCGGCTGCCACTGCCAC 330
QY 82 SerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIleProPhe 101

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Db 331 CTGCGGGTGGTTCAGTGCTCCGACCTGGGTCTGAAGTCTGTGCCCAAGAGATCTCCCT 390
QY 102 AspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluIleLysGluAsnAspPhe 121
Db 391 GACACACCGCTGTGGACCTGCAGAACACAGCATCTCCGAGCTCCGCAAGGATGACTTC 450
QY 122 LysGlyLeuThrSerLeuThrGlyLeuIleLeuAsnAsnAsnLysLeuThrLysIleHis 141
Db 451 AAGGGTCTCCAGCACCTCTACGGCCCTCGTCTGGTGAACAACAAGATCTCCAAGATCCAT 510
QY 142 ProLysAlaPheLeuThrThrLysLysLeuArgArgLeuThrLeuSerHisAsnGlnLeu 161
Db 511 GAGAGGGCTTTCAGCCACCTGCGGAAGCTGCAGAAGCTTACATCTCCAAGAACCACCTG 570
QY 162 SerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsnLys 181
Db 571 GTGGAGATCCGCCCAACCTTACCACCTCCCTGGTGGAGCTCCGATCCACGACACCCG 630
QY 182 ValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGluMet 201
Db 631 ATCCGCAAGGTGCCCAAGGAGTGTTCAGCGGGCTCCGGAACATGAATGCATCGAGATG 690
QY 202 SerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThrVal 221
Db 691 GCGGGAACCCACTGGAGACACTGGCTTGAACCTGGAGCTTCGATGGCTTGAAGCTC 750
QY 222 PheHisIleArgIleAlaGluLysLeuThrSerValProLysGlyLeuProThr 241
Db 751 ACTACTCGGCATCTCAGAGGCCAAGCTGAGCTGGCATCCCAAGACCTCCCTGAGACC 810
QY 242 LeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPheLys 261
Db 811 CTGAATGAACCTCCACCTAGACCACACAAATCCAGGCCATCGAAGGAGCTGCTT 870
QY 262 ArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGluAsn 281
Db 871 CGCTACTCCAAGCTGTACAGCTGGGCTAGGCCACAAACAGATCAGGATGATCGAGAAC 930
QY 282 GlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnLysLeuLys 301
Db 931 GGGAGCTGAGCTTCCTGCCCCACCTCCGGGGAGCTCCACTGGACACAAACAAGTTGGCC 990
QY 302 LysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSerAsn 321
Db 991 AGGGTCCCTCAGGGCTCCAGACCTCAAGCTCTCCAGGTGGTCTATCTGCACCTCAAC 1050
QY 322 SerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysSer 341
Db 1051 AACATCACCACCAAGTGGGTGTCAACGACTTCTGTCCCATGGCTTCGGGTGAAGCGGCC 1110
QY 342 LeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnProAla 361
Db 1111 TACTACAGGCATCAGCTCTTCAACAACCCCGCTCCCTTACTGGGAGGTGCAGCGGCC 1170
QY 362 ThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPhe 377
Db 1171 ACTTCCGCTGCTACTGACCCCTGGCCATCCAGTTGGCAACTAC 1218
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Search completed: May 31, 2003, 15:45:08

Job time : 318 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 31, 2003, 15:15:17 ; Search time 205 Seconds
(without alignments)
2492.831 Million cell updates/sec

Title: US-09-944-884-2

Perfect score: 1992

Sequence: 1 MKEVLLFLALCSAKPFPS.....PATERCVLSRMSVQLGNECM 379

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -DEV=xlh

-MODEL=frame_plus_p2n.model -DEV=xlh

-Q=/cgn2_1/USPTO_spool/US0944884/runat_27052003_150250_7746/app_query.fasta_1.519

-DB=PublishedApplications_NA -QMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1

-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62

-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR_MAX=100

-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0

-MAXLEN=2000000000 -USER=US0944884 -CGN_1_1_57 -runat_27052003_150250_7746

-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100

-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5

-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PublishedApplications_NA:

1:	/cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2:	/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
3:	/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
4:	/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
6:	/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
7:	/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
8:	/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
9:	/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
10:	/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:
11:	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
12:	/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:
13:	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
14:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1992	100.0	2454	9	US-09-944-413-1 Sequence 1, Appli
2	1992	100.0	2454	9	US-09-944-403-1 Sequence 1, Appli
3	1992	100.0	2454	9	US-09-944-896-1 Sequence 1, Appli
4	1992	100.0	2454	9	US-09-944-944-1 Sequence 1, Appli

5	1992	100.0	2454	9	US-09-944-907-1 Sequence 1, Appli
6	1992	100.0	2454	9	US-09-944-929-1 Sequence 1, Appli
7	1992	100.0	2454	9	US-10-028-072-327 Sequence 327, App
8	1992	100.0	2454	9	US-10-121-049-327 Sequence 327, App
9	1992	100.0	2454	9	US-10-123-904-327 Sequence 327, App
10	1992	100.0	2454	9	US-10-140-470-327 Sequence 327, App
11	1992	100.0	2454	9	US-10-175-746-327 Sequence 327, App
12	1992	100.0	2454	9	US-10-176-918-327 Sequence 327, App
13	1992	100.0	2454	9	US-10-176-918-327 Sequence 327, App
14	1992	100.0	2454	9	US-10-137-865-327 Sequence 327, App
15	1992	100.0	2454	9	US-10-140-474-327 Sequence 327, App
16	1992	100.0	2454	9	US-10-142-431-327 Sequence 327, App
17	1992	100.0	2454	9	US-10-143-114-327 Sequence 327, App
18	1992	100.0	2454	9	US-10-140-002-327 Sequence 327, App
19	1992	100.0	2454	9	US-10-142-419-327 Sequence 327, App
20	1992	100.0	2454	9	US-10-123-262-327 Sequence 327, App
21	1992	100.0	2454	9	US-10-142-423-327 Sequence 327, App
22	1992	100.0	2454	9	US-10-121-050-327 Sequence 327, App
23	1992	100.0	2454	9	US-10-141-755-327 Sequence 327, App
24	1992	100.0	2454	9	US-10-143-032-327 Sequence 327, App
25	1992	100.0	2454	9	US-10-123-108-327 Sequence 327, App
26	1992	100.0	2454	9	US-10-123-236-327 Sequence 327, App
27	1992	100.0	2454	9	US-10-123-261-327 Sequence 327, App
28	1992	100.0	2454	9	US-10-140-921-327 Sequence 327, App
29	1992	100.0	2454	9	US-10-140-928-327 Sequence 327, App
30	1992	100.0	2454	9	US-10-121-045-327 Sequence 327, App
31	1992	100.0	2454	9	US-10-123-292-327 Sequence 327, App
32	1992	100.0	2454	9	US-10-123-903-327 Sequence 327, App
33	1992	100.0	2454	9	US-10-124-819-327 Sequence 327, App
34	1992	100.0	2454	9	US-10-124-822-327 Sequence 327, App
35	1992	100.0	2454	9	US-10-140-925-327 Sequence 327, App
36	1992	100.0	2454	9	US-10-160-498-327 Sequence 327, App
37	1992	100.0	2454	9	US-09-944-884-1 Sequence 1, Appli
38	1992	100.0	2454	9	US-10-121-041-327 Sequence 327, App
39	1992	100.0	2454	9	US-10-121-043-327 Sequence 327, App
40	1992	100.0	2454	9	US-10-121-047-327 Sequence 327, App
41	1992	100.0	2454	9	US-10-123-215-327 Sequence 327, App
42	1992	100.0	2454	9	US-10-123-902-327 Sequence 327, App
43	1992	100.0	2454	9	US-10-123-908-327 Sequence 327, App
44	1992	100.0	2454	9	US-10-123-909-327 Sequence 327, App
45	1992	100.0	2454	9	US-10-123-910-327 Sequence 327, App

ALIGNMENTS

RESULT 1
US-09-944-413-1
; Sequence 1, Application US/09944413
; Patent No. US20020156004A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548PICI
; CURRENT APPLICATION NUMBER: US/09/944,413
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25

Db 294 CCTTCACATCCGACTGAAGATATATGCTGCTGAAGATATGGAACACACAGATGATGAT 353
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Db 354 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413
QY 61 ProArgSerHisPhePheProPhePhePhePhePhePhePhePhePhePhePhePhePhePhe 80
Db 414 CCAAGAAGCCATTTTTCATTTGATGCTGCTTCCAAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
QY 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100
Db 474 TATTCAGAGTGTACATGCTCAGATTTAGTTTGCCTCAGTCCCAACCAACATCCCA 533
QY 101 PheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluLysIleLysGluAsnAsp 120
Db 534 TTTGATGACTCGATGCTGCTGCTTCCAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593
QY 121 PheLysGlyLeuThrSerLeuThrGlyLeuIleLeuAsnAsnAsnLysLeuThrLysIle 140
Db 594 TTTAAAGGACTCACTTCACTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 653
QY 141 HisProLysAlaPheLeuThrLysLysLeuArgLeuTyrLeuSerHisAsnGln 160
Db 654 CACCCAAAAGCCTTTCTAACCAAGAAGTTCGGAAGCTGTATCTGCTCCCAATCAA 713
QY 161 LeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180
Db 714 CTAAGTGAATACCACTTAATCTTCCAAATCATTAGCAGAACTCAGAATTCATGAAAT 773
QY 181 LysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGlu 200
Db 774 AAAGTTAAGAAATACAAAGGACACATTCAAAGGAATGAATGCTTTTACACGTTTTGGAA 833
QY 201 MetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThr 220
Db 834 ATGAGTGCAACCTCTTGATATATGATAGAGCCAGGCGCATTTGAGGGGTGACG 893
QY 221 ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProPro 240
Db 894 GTGTTCATATCAGAAATGCAGAAAGCAAACTGACCTCAGTTCTTAAAGGCTTTACCACCA 953
QY 241 ThrLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe 260
Db 954 ACTTTATGAGCTTCCTTAGATTAATAATAAATTTCAACAGTGAACCTTGAGGATTTT 1013
QY 261 LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280
Db 1014 AAACGATACAAAGAACTACAAAGGCTGGCCTAGGAAACAAACAAATCAGATATCGAA 1073
QY 281 AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnAsnLysLeu 300
Db 1074 AATGGAGTCTTGTAAACATACCACTGTCAGAGAAATACATTTGGAACAAATAAATA 1133
QY 301 LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSer 320
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QY 321 AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys 340
Db 1194 AATTCATTTGCAAGAGTGGAGTAATGATCTGCTCCACAGTGCACCAAGATGAAGAAA 1253
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Db 1254 TCTTTATACAGTGAATAAGTTTATTCAACACCCCGGTGAATACTGCGAAATGCAACCT 1313
QY 361 AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet 379
Db 1314 GCAACATTTCTGTTGTTTGGACAGAAATGAGTGTTCAGCTTGGGAACCTTTGGAATG 1370

RESULT 3

US-09-944-896-1

; Sequence 1, Application US/09944896

; Patent No. US20020168715A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT FILING DATE: 2001-08-31
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999

281	QY	AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnAsnLysLeu	300
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301	QY	LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSer	320
1134	Db	AAAAAATCCCTTCAGGATTCACAGATTGAATACTCCAGATAAATCTTCCTTCATTCT	1193
321	QY	AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys	340
1194	Db	AATTCAATTGCAAGAGTGGGAGTAAATGACTTCTGTCCACAGTGCCAAGATGAAGAAA	1253
341	QY	SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnPro	360
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361	c..	AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet	379
1314		GCAACATTCGTTGTTGTTTGGAGCAGAAATGAGTCTCAGCTTGGGAACATTTGGGAATG	1370

RESULT 5

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US-09-944-907-1
; Sequence 1, Application US/09944907
; Publication No. US20020198147A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548PIC1
; CURRENT APPLICATION NUMBER: US/09/944,907
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 1
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-907-1

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Db	774	AAAGTTAAGAAATACAAAAGGACACATTCAAAGGAATGAATGCTTTACACGTTTGGAA	833
Qy	201	MetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThr	220
Db	834	ATGAGTCAAAACCTCTTGATAATAATGGGATAGAGCCAGGGGCATTTGAAGGGGTACG	893
Qy	221	ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProPro	240
Db	894	GTGTTCCATATCAGAAATTCAGAGCAAGCAAACTGCACCTCAGTTCTTAAGGCTTACCACCA	953
Qy	241	ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe	260
Db	954	ACTTTATGGAGCTTCACTTAGATATTAAATAAATTTCAACAGTGGAACTTGAGGATTTT	1013
Qy	261	LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu	280
Db	1014	AAAGGATACAAAGAACTACAAAGGCTGGGCTTAGGAAACAACAAATCACAGATATCGAA	1073
Qy	281	AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnAsnLysLeu	300
Db	1074	AATGGGAGCTTGTCTAACATACCAACGCTGTGAGAGAAATACATTTGGAAAAACAATAACTA	1133
Qy	301	LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSer	320
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Qy	321	AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys	340
Db	1194	AATCAATTCAAGAGTGGGAGTAATGACTTCTGTCCACAGTGCCTGCAAGATGAAGAAA	1253
Qy	341	SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnPro	360
Db	1254	TCTTTATACAGTGCATAAGTTTATTCAACAACCCGGTGAAATACTGGGAAATGCAACCT	1313
Qy	361	AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet	379
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RESULT 7

US-10-028-072-327

; Sequence 327, Application US/10028072

; Publication NO. US20030004311A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang

; TITLE OF INVENTION:

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/028,072

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/049911

; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: 60/056974

; PRIOR FILING DATE: 1997-08-26

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, PRIOR FILING DATE: 1997-12-11
, PRIOR APPLICATION NUMBER: 60/069694
, PRIOR FILING DATE: 1997-12-16
, PRIOR APPLICATION NUMBER: 60/072320
, PRIOR FILING DATE: 1998-01-23
, PRIOR APPLICATION NUMBER: 60/073612
, PRIOR FILING DATE: 1998-02-04
, PRIOR APPLICATION NUMBER: 60/074086
, PRIOR FILING DATE: 1998-02-09
, PRIOR APPLICATION NUMBER: 60/074092
, PRIOR FILING DATE: 1998-02-09
, PRIOR APPLICATION NUMBER: 60/077791
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, PRIOR FILING DATE: 1998-03-20
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, PRIOR FILING DATE: 1998-03-25
, PRIOR APPLICATION NUMBER: 60/079663
, PRIOR FILING DATE: 1998-02-27
, PRIOR APPLICATION NUMBER: 60/079728
, PRIOR FILING DATE: 1998-03-27
, PRIOR APPLICATION NUMBER: 60/080165
, PRIOR FILING DATE: 1998-03-31
, PRIOR APPLICATION NUMBER: 60/081203
, PRIOR FILING DATE: 1998-04-09
, PRIOR APPLICATION NUMBER: 60/081229
, PRIOR FILING DATE: 1998-04-09
, PRIOR APPLICATION NUMBER: 60/081595
, PRIOR FILING DATE: 1998-04-14
, PRIOR APPLICATION NUMBER: 60/081817
, PRIOR FILING DATE: 1998-04-15
, PRIOR APPLICATION NUMBER: 60/081818
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, PRIOR FILING DATE: 1998-04-24
, PRIOR APPLICATION NUMBER: 60/083322
, PRIOR FILING DATE: 1998-04-28
, PRIOR APPLICATION NUMBER: 60/083545
, PRIOR FILING DATE: 1998-04-29
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, PRIOR FILING DATE: 1998-05-07
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, PRIOR FILING DATE: 1998-05-07
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, PRIOR APPLICATION NUMBER: 60/085149
, PRIOR FILING DATE: 1998-05-12
, PRIOR APPLICATION NUMBER: 60/085323
, PRIOR FILING DATE: 1998-05-13
, PRIOR APPLICATION NUMBER: 60/085338
, PRIOR FILING DATE: 1998-05-13
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, PRIOR FILING DATE: 1998-05-13
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, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085697
, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085704
, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/086414
, PRIOR FILING DATE: 1998-05-22
, PRIOR APPLICATION NUMBER: 60/086430
, PRIOR FILING DATE: 1998-05-22
, PRIOR APPLICATION NUMBER: 60/087106
, PRIOR FILING DATE: 1998-05-28
, PRIOR APPLICATION NUMBER: 60/088026
, PRIOR FILING DATE: 1998-06-04
, PRIOR APPLICATION NUMBER: 60/088730
, PRIOR FILING DATE: 1998-06-10
, PRIOR APPLICATION NUMBER: 60/088741
, PRIOR FILING DATE: 1998-06-10
, PRIOR APPLICATION NUMBER: 60/088810
, PRIOR FILING DATE: 1998-06-10

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Score: 1992.00 Matches: 379
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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294 CCTTCACATCGCATGGAAGATATGCTGCAAGGATATGGAAGACACAGATGATGAT 353
QY 41 AspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60
DB 354 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413
QY 61 ProArgSerHisPhePhePhePhePhePhePhePhePhePhePhePhePhePhe 80
DB 414 CCAAGAAGCCATTTTTCATTTGATCTGTTCCCAATGCTCCATTTGGATGCTCAGTGC 473
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DB 474 TATTCACGAGTGTGATATTCATGCTCAGATTTAGGTTTGCCTCAGTCCCAACCATTCGA 533
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DB 534 TTGTGATCTGGAATGCTGATCTTCAAAACATAAATAAATGAAGAAATCAAGAAATGAT 593
QY 121 PheLysGlyLeuThrSerLeuTyrGlyLeuLeuLeuLeuAsnAsnLysLeuThrLysIle 140
DB 594 TTTAAGGACTCACTTCACTTTATGCTGCTGATCTGCTCAACACAAACAACTAAGGAAGAT 653
QY 141 HisProLysAlaPheLeuThrThrLysLysLeuArgLeuTyrLeuSerHisAsnGln 160
DB 654 CACCCAAAAGCCCTTCAACCAACAAAGAGTTGCGAAGGCTGTATCTGTCACCAATCAA 713
C 161 LeuSerGluLeuProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180
714 CTAAGTGAATACCATCTTATCTTCCCAATCATTAGCAACTCAGAACTCATGAAT 773
QY 181 LysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGlu 200
DB 774 AAAGTTAAGAAATACAAAGGACACATCAAGAGGATGAATGCTTTCACCGTTTGGAA 833
QY 201 MetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThr 220
DB 834 ATCAGTGCAAAACCCCTCTGATATAATATGGATAGAGCCAGGGGCATTTGAAGGGGTGACG 893
QY 221 ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProPro 240
DB 894 GTGTTCCATATCAGATTCAGAAAGCAAACTGACCTCAGTTCCTTAAGGCTTACACCA 953
QY 241 ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe 260
DB 954 ACTTTATTGGAGCTTCACCTAGATTAATAAATAATTTCAACAGTGAAGCTTGAGGATTTT 1013
QY 261 LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280
DB 1014 AAACGATACAAAGAACTACAAAGGCTGGGCTAGGAACAAACAAATCACAGATATCGAA 1073
QY 281 AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnAsnLysLeu 300
DB 1074 AATGGGAGTCTTCTAATACATACCAACGCTGTGAGAGAAATACATTTGGAAACAACTAACTA 1133
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DB 1134 AAAAAATCCCTTCAGGATTACAGAGTTGAAATACCTCCAGATAATCTCTTCATTCT 1193
QY 321 AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys 340
DB 1194 AATTCAATTCGAAGAGTGGGAGTAATGACTTCTGTCCAACAGTCCCAAGATGAGAAA 1253
QY 341 SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnPro 360
DB 1254 TCTTTATACAGTCAATAAGTTTATTCAACAACCCGGTGAAATACTGGGAAATGCAACT 1313
QY 361 AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet 379
DB 1314 GCAACATTTTCGTTGTTTGTGAGCAGAAATGAGTGTTCAGCTTGGGAACCTTGGAAATG 1370

RESULT 9
US-10-123-904-327
: Sequence 327, Application US/10123904
: Publication No. US20030022328A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C54
: CURRENT APPLICATION NUMBER: US/10/123,904
: CURRENT FILING DATE: 2002-04-16
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 327
: LENGTH: 2454
: TYPE: DNA
: ORGANISM: Homo Sapien
: US-10-123-904-327

Alignment Scores:
Pred. No.: 1 95e-216 Length: 2454
Score: 1992.00 Matches: 379
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-944-884-2 (1-379) x US-10-123-904-327 (1-2454)
QY 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPheSer 20
DB 234 ATGAAGGAGTATGCTCTCTATTATTCCTGGCTCTGCCAAACCCCTCTTTAGC 293
QY 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40
DB 294 CCTTCACATCGCATGGAAGATATGCTGCAAGGATATGGAAGACACAGATGATGAT 353
QY 41 AspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60
DB 354 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413
QY 61 ProArgSerHisPhePhePhePhePhePhePhePhePhePhePhePhePhePhe 80
DB 414 CCAAGAAGCCATTTTTCATTTGATCTGTTCCCAATGCTCCATTTGGATGCTCAGTGC 473
QY 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100
DB 474 TATTCACGAGTGTGATATTCATGCTCAGATTTAGGTTTGCCTCAGTCCCAACCATTCGA 533
QY 101 PheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluLeuLysGluAsnAsp 120
DB 534 TTGTGATCTGGAATGCTGATCTTCAAAACATAAATAAATGAAGAAATCAAGAAATGAT 593
QY 121 PheLysGlyLeuThrSerLeuTyrGlyLeuLeuLeuLeuAsnAsnLysLeuThrLysIle 140
DB 594 TTTAAGGACTCACTTCACTTTATGCTGCTGATCTGCTCAACACAAACAACTAAGGAAGAT 653
QY 141 HisProLysAlaPheLeuThrThrLysLysLeuArgLeuTyrLeuSerHisAsnGln 160
DB 654 CACCCAAAAGCCCTTCAACCAACAAAGAGTTGCGAAGGCTGTATCTGTCACCAATCAA 713
C 161 LeuSerGluLeuProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180
714 CTAAGTGAATACCATCTTATCTTCCCAATCATTAGCAACTCAGAACTCATGAAT 773
QY 181 LysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGlu 200
DB 774 AAAGTTAAGAAATACAAAGGACACATCAAGAGGATGAATGCTTTCACCGTTTGGAA 833
QY 201 MetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThr 220
DB 834 ATCAGTGCAAAACCCCTCTGATATAATATGGATAGAGCCAGGGGCATTTGAAGGGGTGACG 893
QY 221 ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProPro 240
DB 894 GTGTTCCATATCAGATTCAGAAAGCAAACTGACCTCAGTTCCTTAAGGCTTACACCA 953
QY 241 ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe 260
DB 954 ACTTTATTGGAGCTTCACCTAGATTAATAAATAATTTCAACAGTGAAGCTTGAGGATTTT 1013
QY 261 LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280
DB 1014 AAACGATACAAAGAACTACAAAGGCTGGGCTAGGAACAAACAAATCACAGATATCGAA 1073
QY 281 AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnAsnLysLeu 300
DB 1074 AATGGGAGTCTTCTAATACATACCAACGCTGTGAGAGAAATACATTTGGAAACAACTAACTA 1133
QY 301 LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSer 320
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Db 774 AAAGTTAAAGAAATACAAAAGGACACATTCAAAGGAATCAATGCTTTACACGTTTGGAA 833
Qy 201 MetSerAlaAsnProLeuAspAsnGlyIleGluProGlyAlaPheGluGlyValThr 220
Db 834 ATGAGTGGAAACCTCTTGATATTAATGGATAGAGCCAGGGCAATTTGAAGGGTGAGC 893
Qy 221 ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuPro 240
Db 894 GTGTTCCATATCAGAAATGCAGAACAAACCTCAGTTCCTTAAAGGCTTACCACCA 953
Qy 241 ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe 260
Db 954 ACTTTATTGGAGCTTCACCTAGATTATATAAATTTCAACAGTGGAACTTGAGGATTTT 1013
Qy 261 LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280
Db 1014 AARCATCAAGAAGAACTACAAGGCTGGCCCTAGGAACAACAATAACACATATCGAA 1073
Qy 281 AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnLysLeu 300
Db 1074 AATGGAGCTCTGTACATACCACGCTGTGAGAGAAATACATTTGGAAACAATAAACA 1133
Qy 301 LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIlePheLeuHisSer 320
Db 1134 AAAAAAATCCCTTCAGGATTACACAGATTGAAATACCTCCAGATAATCTTCTTCAATCT 1193
Qy 321 AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys 340
Db 1194 AATCAATGTGCAAGAGTGGAGTAATGACCTCTGTCCACAGAGTGCACCAAGATGAGAA 1253
Qy 341 SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnPro 360
Db 1254 TCTTTATACAGTGCATAAGTTTATTCAACACCCGGTGAAATCTCTGGGAAATGCAACCT 1313
Qy 361 AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet 379
Db 1314 GCAACATTCGTTGTGTTTGGACGAAATGAGTGTTCAGCTTGGGAACCTTTGGAAATG 1370

RESULT 11

US-10-175-746-327
; Sequence 327, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 327
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-746-327

Alignment Scores:

Pred. NO.: 1.95e-216 Length: 2454
Score: 1992.00 Matches: 379
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-944-884-2 (1-379) x US-10-175-746-327 (1-2454)
Qy 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPhePheSer 20
Db 234 ATGAAGAGTAGTAGTCTCTATTATTCCTGGCTCTGCGAAACCCCTCTTTTAGC 293
Qy 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40
Db 294 CCTTCACACATCGCACTGAAGATATGATGCTGAAGGATATGGAAGACACAGATGAT 353
Qy 41 AspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60
Db 354 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 413
Qy 61 ProArgSerHisPhePheProPheAspLeuPheProMetCysProPheGlyCysGlnCys 80
Db 414 CCAAGAAGCCATTTTTCCTATTTGATCTGTTCATATGTTCATATGTTCATATGTTC 473
Qy 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100
Db 474 TATTCACACAGTGTACATGCTCAGATTTAGTTTGACCTCAGTCCCAACCAACATTC 533
Qy 101 PheAspThrArgMetLeuAspLeuGlnAsnLysIleLysGluIleLysGluAsnAsp 120
Db 534 TTTGATACTCGAATGCTTGATCTTCAAAACAATAAATAAGGAAATCAAGAAATGAT 593
Qy 121 PheLysGlyLeuThrSerLeuTyrGlyLeuIleLeuAsnAsnLysLeuThrLysIle 140
Db 594 TTTAAAGGACTCACCTTCATCTTATGCTGTGATCTCTGAACCAACAACAGCTACGAG 653
Qy 141 HisProLysAlaPheLeuThrThrLysLysLeuArgArgLeuTyrLeuSerHisAsnGln 160
Db 654 CACCCAAAAGCCTTCTTAACCAAAAGAGTTGGCAAGCTGTATCTGTCCCAACATCAA 713
Qy 161 LeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180
Db 714 CTAAGTGAATACCACCTTAATCTTCCCAATCATTAGCAGAACTCAGAAATTCATG 773
Qy 181 LysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGlu 200
Db 774 AAAGTTAAAGAAATACAAAAGGACACATTCAAAGGAATGAATGCTTTACACGTTTGG 833
Qy 201 MetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThr 220
Db 834 ATGAGTGCACACCTCTTGATATTAATGGATAGAGCCAGGGGCATTTGAAGGGTGAGC 893
Qy 221 ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuPro 240
Db 894 GTGTTCCATATCAGAAATGCAGAACAAACCTCAGTTCCTTAAAGGCTTACCACCA 953
Qy 241 ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe 260
Db 954 ACTTTATTGGAGCTTCACCTAGATTATATAAATTTCAACAGTGGAACTTGAGGATTTT 1013
Qy 261 LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280
Db 1014 AARCATCAAGAAGAACTACAAGGCTGGCCCTAGGAACAACAATAACACATATCGAA 1073
Qy 281 AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnLysLeu 300
Db 1074 AATGGAGCTCTGTACATACCACGCTGTGAGAGAAATACATTTGGAAACAATAAACA 1133
Qy 301 LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIlePheLeuHisSer 320
Db 1134 AAAAAAATCCCTTCAGGATTACACAGATTGAAATACCTCCAGATAATCTTCTTCAATCT 1193


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QY 321 AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys 340
Db 1194 AATTCAAATTCGAAGAGTGGAGTAATGACTTCTGTCACACAGTGCCAAAGATGAAGAAA 1253
QY 341 SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnPro 360
Db 1254 TCTTTATACAGTGCATAGATTATTATCAACACCCGGTGAATATACTGGGAATGCAACT 1313
QY 361 AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet 379
Db 1314 GCAACATTTTCGTTGTTTGTGAGCAGATGAGTGTTCAGCTGGGAACCTTTGGAATG 1370
RESULT 12
US-10-176-918-327
; Sequence 327, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 327
; TYPE: DNA
; LENGTH: 2454
; ORGANISM: Homo Sapien
US-10-176-918-327
Alignment Scores:
Pred. No.: 1,95e-216 Length: 2454
Score: 1992.00 Matches: 379
Percent Similarity: 100.00% Conservative: 0
c Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-944-884-2 (1-379) x US-10-176-918-327 (1-2454)
QY 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPhePheSer 20
Db 234 ATGAAGAGATGTGCTCTCTATTATTCCTGGCTTGTGCTCGCCAAACCCCTCTTTAC 293
QY 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40
Db 294 CCTTCACATCGCACTGAAGAATATGATGCTGAAGGATATGAAGACACACAGATGATGAT 353
QY 41 AspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60
Db 354 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413
QY 61 ProArgSerHisPhePheProPheAspLeuPheProMetCysProPheGlyCysGlnCys 80
Db 414 CCAGAAGGCCATTTTTTTCATTTGATCTGTTTCCCAATGTGTCATTTGGATGTCAGTGC 473
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QY 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100
Db 474 TATTCACGAGTGTGATCATTTGCTCAGATTTAGGTTCACCTAGTCCCAACCAACATTTCCA 533
QY 101 PheAspThrArgMetLeuAspLeuGlnAsnLysIleLysGluIleLysGluAsnAsp 120
Db 534 TTTGATACCTCGATGCTTGTGATCTTCAAAACATAAAATTAAGGAATCAAGAAATGAT 593
QY 121 PheLysGlyLeuThrSerLeuTyrGlyLeuIleLeuAsnAsnLysLeuThrLysIle 140
Db 594 TTTAAAGGACTCACTTCATCTTATGCTGATCTCTGATCCTGAACAACAACAAGCTAACGAAGAT 653
QY 141 HisProLysAlaPheLeuThrLysLysLeuArgLeuLeuSerHisAsnGln 160
Db 654 CACCCCAAAAGCCCTTCTTAACCAAAAGAGTTCGGAAGGCTGTATCTGTCCCAACATAA 713
QY 161 LeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180
Db 714 CTAAGTGAATACCACTTAACTTCCCAATCATTAGCAGAACTCAGAAATTCATGAAT 773
QY 181 LysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGlu 200
Db 774 AAAGTTAAGAAAATACAAAAGGACACATTCAAAGGAATGAATGCTTTACACGCTTTTGGAA 833
QY 201 MetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThr 220
Db 834 ATGAGTGCAACCCCTCTTATATAATGGGATAGAGCCAGGGGCATTTGAAGGGGTGAGC 893
QY 221 ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuPro 240
Db 894 GTGTTCCATATCAGAATTCAGAGAGCAAACTGACCTCAGTCTCTAAAGGCTTTACACCA 953
QY 241 ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe 260
Db 954 ACTTTATTGGAGCTTCACCTAGATTTATATAAAATTTCAACAGTGGAACTTGAGGATTT 1013
QY 261 LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280
Db 1014 AAACGATACAAGAACTACAAAGGCTGGGCCTAGGAAACAACAATAATCAGATATCGAA 1073
QY 281 AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnAsnLysLeu 300
Db 1074 AATGGAGTCTTCTAACATACCCCGTGTGAGAGAAATACATTTGGAAACAATAACTA 1133
QY 301 LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSer 320
Db 1134 AAAAAATCCCTTCAGGATTACCAGAGTTGAATACTCCAGATATCTTCTTCATTCT 1193
QY 321 AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys 340
Db 1194 AATTCAAATTCGAAGAGTGGAGTAAATGACTTCTGTCACACAGTGCACAAAGATGAAGAAA 1253
QY 341 SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnPro 360
Db 1254 TCTTTATACAGTGCATAATAAGTTTATTCAACAACCCCGTGAATATCTGGGAATATGCAACCT 1313
QY 361 AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet 379
Db 1314 GCAACATTTTCGTTGTTTGTGAGCAGATGAGTGTTCAGCTGGGAACCTTTGGAATG 1370
RESULT 13
US-10-176-921-327
; Sequence 327, Application US/10176921
; Publication No. US20030027276A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
```


Score: 1992.00 Matches: 379
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-944-884-2 (1-379) x US-10-137-865-327 (1-2454)

QY 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPhePheSer 20
DB 234 ATGAAGGAGTATGTCCTCTATTATTCCTGGCTTTGCTGCAACCCCTCTTTAGC 293

QY 21 ProSerHisLeuAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40
DB 294 CCTTCACATCGCAGCTGAAGATATGCTGAAGATATGGAAGACACAGATGATGAT 353

QY 41 AspAspAspAspAspAspAspAspAspAspAspAspAspAspAspAspAspAsp 60
DB 354 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413

QY 61 ProArgSerHisPhePhePhePhePhePhePhePhePhePhePhePhePhePhe 80
DB 414 CCAAGAAGCCATTTTTCATTTGATCTGTTTCCAAATGTTCCATTTGGATGTCAGTGC 473

QY 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100
DB 474 TATTCAGGAGTGTACATGCTCAGATTTAGTTTGGCTGAGTCCCAACCAATTCCTCA 533

QY 101 PheAspThrArgMetLeuAspLeuGlnAsnLysLysLysLysLysLysLysLysLys 120
DB 534 TTTGATGACTCGAATGCTGTCTTCAAAACAATAAATTAAGGAATCAAAAGAAATGAT 593

QY 121 PheLysGlyLeuThrSerLeuTyrGlyLeuLysLeuAsnAsnAsnLysLeuThrLysIle 140
DB 594 TTTAAGGAGTCACTTCCATTTATGTTGCTGATCTGATCTGATCAACAACAAGTAAACGAAGATT 653

QY 141 HisProLysAlaPheLeuThrThrLysLysLeuArgLeuTyrLeuSerHisAsnGln 160
DB 654 CACCAAAAGCCCTTCTTAACACAAAGAGTTGCGAAGGCTGATCTGCTCCCAACAA 713

QY 161 LeuSerGluLeuProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180
DB 714 CTAAGTGAATACCACTTAATCTTCCCAATCATTAGCAGAACTCAGAAATCATGAAAT 773

QY 181 LysValLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 200
DB 774 AAAGTTAAGAAATACAAAGGACACATTCAAAGGAATGAATGCTTTACAGCTTTTGGAA 833

QY 201 MetSerAlaAsnProLeuAspAsnAsnGlyLeuGluProGlyAlaPheGluGlyValThr 220
DB 834 ATGAGTGCAAAACCCCTCTTGATATATATGATAGAGCCAGGGCATTTGAAGGGGTGACG 893

QY 221 ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProPro 240
DB 894 GTGCTTCATATCAGAAATTCAGAAAGCAAACTGACCTCAGTTCTTAAAGGCTTACCACCA 953

QY 241 ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe 260
DB 954 ACTTTATGAGGCTTCACTTAGATTAATAAATTTCAACAGTGAACCTTGAGGATTTT 1013

QY 261 LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280
DB 1014 AAACGATACAAAGAACTCAAAAGGCTGGGCTTAGGAAACAAACAAATTCAGATATCGAA 1073

QY 281 AsnGlySerLeuAlaAsnIleProArgValArgGluLysLysLysLysLysLysLysLys 300
DB 1074 AATGGGAGTCTTCTTAACATACCACTGTCAGAGAAATACATTTGGAAAAACAATAAATA 1133

QY 301 LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSer 320
DB 1134 AAAAAATCCCTTCAGAGATTACCAAGAGTTGAAATACCTCCAGATAATCTTCTTCATTCT 1193

QY 321 AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys 340

DB 1194 AATTCATTTGCAAGAGTGGGAGTAATGACTTCTGTCAACAGTGCACCAAGATGAAGAA 1253

QY 341 SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnPro 360

DB 1254 TCTTTATACAGTGCATAAAGTTTATTCAACAACCCGCGTGAATACTGGGAAATCAACCT 1313

QY 361 AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet 379

DB 1314 GCAACATTTCTGTTGTTTGGAGAGAATGAGTGTTCAGCTTGGCAACTTTTGAATG 1370

RESULT 15

US-10-140-474-327

; Sequence 327, Application US/10140474

; Publication No. US20030032156A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Collin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330R1C162

; CURRENT APPLICATION NUMBER: US/10/140,474

; CURRENT FILING DATE: 2002-05-06

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 327

; LENGTH: 2454

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-140-474-327

Alignment Scores:

Pred. No.: 1,95e-216 Length: 2454

Score: 1992.00 Matches: 379

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-944-884-2 (1-379) x US-10-140-474-327 (1-2454)

QY 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPhePheSer 20

DB 234 ATGAAGGAGTATGTCCTCTATTATTCCTGGCTTTGCTGCAACCCCTCTTTAGC 293

QY 21 ProSerHisLeuAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40

DB 294 CCTTCACATCGCAGCTGAAGATATGCTGAAGATATGGAAGACACAGATGATGAT 353

QY 41 AspAspAspAspAspAspAspAspAspAspAspAspAspAspAspAspAspAsp 60

DB 354 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413

QY 61 ProArgSerHisPhePhePhePhePhePhePhePhePhePhePhePhePhePhe 80

DB 414 CCAAGAAGCCATTTTTCATTTGATCTGTTTCCAAATGTTCCATTTGGATGTCAGTGC 473

QY 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100

Mon Jun 2 10:28:59 2003

[illegible]

Search completed: May 31, 2003, 17:13:37
Job time : 217 secs